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(74) Common Representative: NOVOZYMES A/S;
Krogshøjvej 36, DK-2880 Bagsværd (DK).

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(71) Applicant (*for all designated States except US*):
NOVOZYMES A/S [DK/DK]; Krogshøjvej 36, DK-2880
Bagsværd (DK).

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(72) Inventors; and

(75) Inventors/Applicants (*for US only*): ANDERSEN,
Jens, Tønne [DK/DK]; Alfred Christensens Vej 35,
DK-2850 Nærum (DK). JØRGENSEN, Steen, Troels
[DK/DK]; Prunusvej 5, DK-3450 Allerød (DK). RAS-
MUSSEN, Michael, Dolbjerg [DK/DK]; Syvbjergvej
151, DK-2625 Vallensbæk (DK). OLSEN, Peter, Bjarke
[DK/DK]; Svendborggade 8, 4 tv, DK-2100 Copenhagen
Ø (DK). CLAUSEN, Ib, Groth [DK/DK]; Fyrrestien 6,
DK-3400 Hillerød (DK).

(54) Title: IMPROVED BACILLUS HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell, derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions

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Improved Bacillus Host Cell

TECHNICAL FIELD

Bacillus sp. are attractive hosts for the production of heterologous proteins due their ability to secrete proteins directly into the culture medium. They have a high capacity for protein secretion, are genetically highly amenable, nonpathogenic and free of endotoxins, and consequently a large variety of proteins from different organisms have been efficiently produced and secreted in *Bacillus sp. i.e. in Bacillus licheniformis*. In the highly competitive biotech industry, even slightly improved *Bacillus* host cells are in demand, which may provide more attractive production systems, or may even just be alternative production systems.

BACKGROUND

Many industrial products of commercial interest can be produced biologically in *Bacillus sp.* host cells e.g. heterologous polypeptides, amino acids, carbohydrates etc. Some of these products are sold as process aids, intermediates, or even end-products in the food and feed industries as well as in the pharmaceutical industry. There are increasingly strict regulations that must be complied with when producing such products in microbial production hosts for sale in these industries, for instance the presence of bacterial spores in the products is seen as a problem. When producing in *Bacillus licheniformis* it is thus desirable to ensure that the host cell is not capable of forming spores.

SUMMARY

A problem to be solved by the present invention is how to obtain a *Bacillus licheniformis* host cell incapable of forming spores, or how to impair the sporulation process of said cell. The present invention provides a solution to the problem by providing a *Bacillus licheniformis* host cell which has a reduced capacity to produce one or more polypeptide(s) involved in sporulation.

Accordingly, in a first aspect the invention relates to a *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129 (both included), or in SEQ ID NO's: 2 to 191 (both included), preferably at least 85% identical, more preferably at least 90% identical, still more preferably at least 95% identical, and most preferably at least 97% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129 (both included), or in SEQ ID NO's: 2 to 191 (both included), wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than

the parent host cell, when they are cultivated under comparable conditions. Preferably the mutant host cell expresses at least 10% less, more preferably at least 20% less, still more preferably at least 30% less, even more preferably at least 40% less, yet more preferably at least 50% less, or at least 60% less, or at least 70% less, or at least 80%, or most preferably at least 90% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions. Most preferably the mutant host cell expresses absolutely nothing of the one or more polypeptide(s) involved in sporulation.

Comparable conditions of cultivation must be used in order to compare the expression level of the one or more polypeptide(s) involved in sporulation in a mutant host cell of the invention with that in a parent host cell. They are cultivated separately under identical conditions in identical setups, of course allowing for the usual standard deviations of the operating parameters normally associated with growth experiments, such as temperature control etc.

The quantification of the expression level of the one or more polypeptide(s) is done by standard text-book assay techniques as known in the art e.g. mRNA quantification or immuno-based assays.

In a second aspect the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the previous aspect in a suitable medium, whereby the said product is produced.

Finally, an aspect of the invention relates to a use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

DEFINITIONS

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present

invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

Coding sequence: When used herein the term "coding sequence" is intended to cover a nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

Expression: In the present context, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Expression vector: In the present context, the term "expression vector" covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

DETAILED DISCLOSURE

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191 (both included), wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

The term "parent host cell" in the context of the present invention means a cell which is genetically identical, or isogenic, to the progeny mutant or mutant cell of the present

invention, except for the mutated one or more gene(s) encoding one or more polypeptide(s) involved in sporulation in said mutant.

5 The degree of identity, or %-identity of polypeptide sequences can suitably be investigated by aligning the sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP
10 creation penalty of 5.0 and GAP extension penalty of 0.3".

15 An object of the present invention is to provide a culture medium free of bacterial spores so as to reduce the product purification to a minimum, and to comply with regulatory requirements. This may be done according to the invention by reducing or even completely abolishing the expression of one or more gene(s) encoding a native polypeptide(s) involved in sporulation via mutagenisation of that (those) gene(s). One of the very well-known method of ensuring that a gene is not expressed into an active polypeptide within a cell is simply to delete or partially delete the encoding gene. Many techniques have been described in the art on how to specifically delete or partially delete one or more gene(s) in the genome of a cell,
20 and certainly from the genome of a *Bacillus licheniformis* cell (see e.g. Novozymes A/S WO 01/90393, Novozymes A/S WO 02/00907). Accordingly, a preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.

25 A preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.

30 The product of interest to be produced by the mutant host cell of the first aspect may be one or more polypeptide(s) encoded by one or more heterologous gene(s). Consequently, a preferred embodiment of the present invention relates to a host cell of the first aspect, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

35 In the industrial production of polypeptides it is of interest to achieve a product yield as high as possible. One way to increase the yield is to increase the copy number of a gene

encoding a polypeptide of interest. This can be done by placing the gene on a high copy number plasmid. However, plasmids are unstable and are often lost from the host cells if there is no selective pressure during the cultivation of the host cells. Another way to increase the copy number of the gene of interest is to integrate it into the host cell chromosome in multiple copies. Integration of two genes has been described in WO 91/09129 and WO 94/14968 (Novozymes A/S) the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) is present in at least two copies, preferably at least 4 copies, and most preferably at least 6 copies. In another embodiment the heterologous gene(s) is present in at least ten copies. If carried on a plasmid the gene(s) may be present in several hundred copies per cell, so in a still further embodiment of the present invention the heterologous gene(s) is present in at least 100 copies.

Integration of two genes closely spaced in anti-parallel tandem to achieve better stability has been described in WO 99/41358 (Novozymes A/S) the content of which is hereby incorporated by reference, as well as the stable chromosomal multi-copy integration of genes described in WO 02/00907 (Novozymes A/S) the content of which is incorporated herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

Selection of chromosomal integrant has for convenience resulted in the use of selectable markers such as antibiotic resistance markers. However it is desirable if possible to avoid the use of antibiotic marker genes. WO 01/90393 discloses a method for the integration of a gene in the chromosome of a host cell without leaving antibiotic resistance markers behind in the strain, the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker gene(s) at the site of integration.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence encoding a product of interest, which may be operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A nucleotide sequence encoding a polypeptide of interest may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the expression

vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

Other ways of increasing the product yield would be to increase promoter activity of the specific promoter regulating the expression of a specific gene of interest. Also a more general increase in the activity of several promoters at the same time could lead to an improved product yield. The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli* lac operon, *Streptomyces coelicolor* agarase gene (*dagA*), *Bacillus subtilis* levansucrase gene (*sacB*), *Bacillus licheniformis* alpha-amylase gene (*amyL*), *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), *Bacillus licheniformis* penicillinase gene (*penP*), *Bacillus subtilis* *xylA* and *xylB* genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, Proceedings of the National Academy of Sciences USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proceedings of the National Academy of Sciences USA 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242: 74-94; and in Sambrook et al., 1989, supra.

Other useful promoters are described in WO 93/10249, WO 98/07846, and WO 99/43835 (Novozymes A/S) the contents of which are incorporated fully herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

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The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

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The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

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Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

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The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding

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region may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* laccase (WO 95/33836).

- 5 Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.
- 10 It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In
- 15 yeast, the ADH2 system or GAL1 system may be used. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.
- 20 The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide
- 25 sequence of the present invention may be expressed by inserting the nucleotide sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.
- 30 The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.
- 35 The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication,

e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance.

The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM β 1 permitting replication in *Bacillus*. The origin of replication may be one having a mutation which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75: 1433).

More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, *supra*).

The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Molecular General Genetics* 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, *Journal of Bacteriology* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *Journal of Molecular Biology* 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *Journal of Bacteriology* 169: 5771-5278).

A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon. The term "operon" in the context of the present invention means a polynucleotide comprising several genes that are clustered and perhaps even transcribed together into a polycistronic mRNA, e.g. genes coding for the enzymes of a metabolic pathway. The transcription of an operon may be initiated at a promoter region and controlled by a neighboring regulatory gene, which encodes a regulatory protein, which in turn binds to the operator sequence in the operon to respectively inhibit or enhance the transcription. The

gene or the operon can be carried on a suitable plasmid that can be stably maintained, e.g. capable of stable autonomous replication in the host cell (the choice of plasmid will typically depend on the compatibility of the plasmid with the host cell into which the plasmid is to be introduced) or it can be carried on the chromosome of the host. The said gene may be
5 endogenous to the host cell in which case the product of interest is a protein naturally produced by the host cell and in most cases the gene will be in its normal position on the chromosome. If the gene encoding the product of interest is an exogenous gene, the gene could either be carried on a suitable plasmid or it could be integrated on the host chromosome. In one embodiment of the invention the eubacterium is a recombinant
10 eubacterium. Also the product of interest may in another embodiment be a recombinant protein.

The product of interest is any gene product or product of a metabolic pathway which is industrially useful and which can be produced in a bacterial cell such as a *B. licheniformis*.

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In one preferred embodiment, the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

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In another preferred embodiment, the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

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Yet another embodiment relates to a host cell of the first aspect, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants, and preferably the carbohydrates comprise hyaluronic acid.

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In one embodiment the heterologous polypeptide(s) is an enzyme, particularly the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). Preferably the enzyme is an enzyme with an activity selected
35 from the group consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Preferably the enzyme is an amylase or a mannanase.

A second aspect of the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the first aspect of the invention in a suitable medium, whereby the said product is produced. One embodiment relates to a process of the second aspect, further comprising isolating or purifying the product of interest. Suitable media for the cultivation is described below as well as methods for the purification or isolation of the produced product which is an optional additional step to the process of the present invention.

In the production methods of the present invention, the cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The medium used to culture the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared using procedures known in the art (see, e.g., references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

The resulting polypeptide may be recovered by methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures

including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

5 The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

10 A third aspect of the present invention relates to the use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced, and optionally isolating or purifying the produced product.

CLAIMS

1. A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 191, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.
2. The host cell according to claim 1, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.
3. The host cell according to any of claims 1 – 2, which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.
4. The host cell according to any of claims 1 – 3, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).
5. The host cell according to claim 4, wherein the heterologous gene(s) is present in at least two copies.
6. The host cell according to claim 4 or 5, wherein the heterologous gene(s) are stably integrated into the genome of the cell.
7. The host cell according to any of claims 4 - 6, wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes at the site of integration.
8. The host cell according to any of claims 4 - 7, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.
9. The host cell according to any of claims 4 – 8, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon.
10. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

11. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

12. The host cell according to claim 11, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants.

13. The host cell according to claim 12, wherein the carbohydrates comprise hyaluronic acid.

14. The host cell according to any of claims 4 – 9, wherein the heterologous polypeptide(s) is an enzyme, preferably a secreted enzyme.

15. The host cell according to claim 14, wherein the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6).

16. The host cell according to claim 15, wherein the enzyme is an enzyme with an activity selected from the group of enzyme activities consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, and xylanase.

17. The host cell according to claim 16, wherein the enzyme is an amylase or a mannanase.

18. A process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in any of the claims 1 - 17 in a suitable medium, whereby the said product is produced.

19. The process according to claim 18, further comprising isolating or purifying the product of interest.

20. A use of a *Bacillus licheniformis* mutant host cell as defined in any of the claims 1 - 17 for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

21. The use according to claim 20 further comprising isolating or purifying the product of interest.

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Jørgensen, Steen Troels
Olesen, Peter Bjarke
Andersen, Jens Tønne
Rasmussen, Michael Dolberg

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Asn Pro Glu Phe Leu Val Gly Asp Pro Glu Glu

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10295.204.ST25.txt
180

175

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accgccctag tttctttttt ttcagcacga atctttatgg tataatgagt gttggaatca 1126
atagaaacgt ttatacatag tgagggatta aatatggcag gctacacgcc tatgatacag 1186
caatatttaa agattaaggc agagtatcag gatgcctttt tatttttttcg tcttggcgac 1246
ttttatgaga tgttttttga agatgcaaaa aaggcgtctc aggagctcga aatcacgctg 1306
acgagcaggg acggaggatc aagcgaaaga attccgatgt gcgggggttcc ttatcattcc 1366
tgctcttcgt atatcgaaca gctcattaaa aaaggctata aagtcgcat ctgtgaacag 1426
gtggaggacc ctaaatcggc caaaggagtc gtcaaaaggg aagtcgtgca gctgatcaca 1486
cccggcaccg tgatggacgg caaagggtt catgaaaatg aaaacaactt tatcgcttct 1546
gtc 1549

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<210> 8
 <211> 182
 <212> PRT
 <213> Bacillus licheniformis

<400> 8

Met Ser Glu Tyr Arg Glu Ile Ile Thr Lys Ala Val Val Ala Lys Gly
1 5 10 15

Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser Pro Ser Gln Lys Pro
20 25 30

Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His Lys Tyr Asp Ala Glu
35 40 45

Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val
50 55 60

Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg
65 70 75 80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr
85 90 95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn
100 105 110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln
115 120 125

Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val
130 135 140

Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp
145 150 155 160

val Gly Asp Pro Glu Glu
180

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<210> 9
<211> 1477
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501)..(974)
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[illegible]

10295.204.ST25.txt

Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn
 125 130 135

ctc gtc gac ctg cta aaa ggc gac gcc atg cat gcg caa aaa gcg ata 965
 Leu Val Asp Leu Leu Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile
 140 145 150 155

tcg atg aga taaaaaagcc agcgaggata gaatcctcac tggctctggt 1014
 Ser Met Arg

ttttgctatt ttacgattaa aaccggacac ttactcttt tcgccacttt atggctgaca 1074
 cttccgagca ccatttcctg caaagtgttc agccccctgc ttccgataat cacgatatca 1134
 acatcatgat ggttggcgta cgatacaatg gccgggcccg gatccccgtg ctgcatcgtc 1194
 atttgatagg gaacggccgc ctgttttaat ttattttcta tcgacagcag cctgctgcgc 1254
 cgttcgcggt cgagttctgt acggttttcg ctatgcagga cttcatgttt tgctctcgca 1314
 taatccaata cataaatcat gtcgacgacc gcttcgtttg acatggaagc cagatgaatc 1374
 gcatgatcgg cagctctttc agaatgcttg gaaccgtcag cagccagcag tatatgtcta 1434
 tacacccttc atcaccggt tcttagtgat ttgacactga acg 1477

<210> 10
 <211> 158
 <212> PRT
 <213> Bacillus licheniformis

<400> 10

Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr Leu Glu Leu His Glu
 1 5 10 15

Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys Ile Lys Lys Ser Met
 20 25 30

Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala
 35 40 45

Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys
 50 55 60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp
 65 70 75 80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala
 85 90 95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val
 100 105 110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe
 115 120 125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu
 Page 12

10295.204.ST25.txt
140

130

135

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg
 145 150 155

<210> 11
 <211> 1752
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (183)..(1256)

<400> 11
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 acatacgcgc cgtaaagaca agtgtactga ggcaaatgac tgtttttggt caaacttagg 120
 cggctctgctt ccgggacagg tttttttcac atatgatatg tcagctgaaa aaggaggaaa 180
 tg atg atg agt gcc act gcc ttg ccg gcc ttt agg ctg cac att cat 227
 Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His 15
 1 5 10
 ccg aag cat ctg ctt gag ttg aaa aaa gac gtc tgg agt gat gaa gcc 275
 Pro Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala 30
 20 25
 gtt ccc ggc atg ctc ttg acc ggt tca gca aag acg cct gtc gca gtg 323
 Val Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val 45
 35 40
 tca tac aga ggg gcc cac acc cgc aaa ctg acg aaa aaa tcc tat ttc 371
 Ser Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe 60
 50 55
 att caa tat ccg gac aat aaa gaa aag gct gcg ttt cat ttg aac gcg 419
 Ile Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala 75
 65 70
 gaa tat cat gat ccg tct ttc atc aga aac agg ctt tcc ttt cat ttt 467
 Glu Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe 90
 80 85
 ttt gaa caa atc ggc gtc ctt gcg cca gca gca tca cac gtt ttc ctt 515
 Phe Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu 110
 100
 tat atc aat gaa aaa aaa gaa ggc atc tat tta aaa atc gaa tct gtt 563
 Tyr Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val 125
 115 120
 gac gat cat ttc tta aag agg aga aat tta gaa agg ggg gcc att tat 611
 Asp Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr 140
 130 135
 tat gcc gtt gat gac gat gct aat ttt tct ctg ctg agt tcc ttc aat 659
 Tyr Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn 155
 145 150
 aaa aag gct aag caa aat ctc atg cag gga tac gaa aga aaa acg ggt 707
 Lys Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly 175
 160 165 170

10295.204.ST25.txt

tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat	755
Ser Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn	
180 185 190	
acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat	803
Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp	
195 200 205	
gtc aaa caa tat ttg ctg tgg ctc atc ggc gcc gtc tgc acc caa aat	851
Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn	
210 215 220	
ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca	899
Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr	
225 230 235	
aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cgg	947
Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg	
240 245 250 255	
aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc	995
Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly	
260 265 270	
tat aat acg ctg tct gca agg ctg ctc gac atc ccg gct ttt caa tcc	1043
Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser	
275 280 285	
caa tac ttt aat tta atg aaa aat gtc ttg cac cgc caa ttt aca atc	1091
Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile	
290 295 300	
agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct	1139
Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro	
305 310 315	
ttt ctt gaa cat gat cct tat aca acc gtc aca tac agc cgg ctc gaa	1187
Phe Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu	
320 325 330 335	
gat gag caa aaa caa att ttt cat ttc atc gat cag agg aag cgg ttc	1235
Asp Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe	
340 345 350	
ctg ctt ttc gag ctt tcc cga taatagactg tcgctgtcct ccgaaaaaaa	1286
Leu Leu Phe Glu Leu Ser Arg	
355	
tggtcacattt tttgtcatat tggcgaaaaa aatccctttt acacaaaata aggtatacta	1346
gcaatatcaa ggacatcaat gcgctgaata cctgaaatta ccgactcaaa atacaaatcg	1406
aaagttggag actgccatga tgaacaataa aattgaagca aaaagactgg ctttatttga	1466
agctgcccga aagttcggca tcaactccaa agaggccatt cgatgcagtc aggaattgga	1526
caacttgctg aatcaaagaa tgcaaaagga tgataactgc gtgcatgcgg aagaaagaaa	1586
aggccgccac acgtcatgac ctccgactgc aagctgcgcc tgatgccggc ctccttcctc	1646
ctccatttca tcatccgttg atttcgggtc gcagcttggg ctattcggcc attgtttttt	1706
gaacataaat catcgtgcaa ataccgtagg caagaatggc tgaagg	1752

<210> 12
 <211> 358
 <212> PRT

10295.204.ST25.txt

<213> Bacillus licheniformis

<400> 12

Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His Pro
 1 5 10 15
 Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala Val
 20 25 30
 Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val Ser
 35 40 45
 Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
 50 55 60
 Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu
 65 70 75 80
 Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe
 85 90 95
 Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr
 100 105 110
 Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp
 115 120 125
 Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr
 130 135 140
 Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys
 145 150 155 160
 Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser
 165 170 175
 Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr
 180 185 190
 Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val
 195 200 205
 Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe
 210 215 220
 Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys
 225 230 235 240
 Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn
 245 250 255

10295.204.ST25.txt

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr
 260 265 270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln
 275 280 285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser
 290 295 300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe
 305 310 315 320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp
 325 330 335

Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe Leu
 340 345 350

Leu Phe Glu Leu Ser Arg
 355

<210> 13
 <211> 1570
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1067)

<400> 13
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 aaaagatact acagaacccc tccaaatcta tatctagggtt tttagccccc cggccttccg 120
 cagttttccc cgatggaggc gctgcaaaaa gggacgcttt ggcccgtatt ttacgatcat 180
 tatgaaaatc cgtatgaaga tgggaggtaa ggagggtgac gaactcttta ccgcaagact 240
 attataaaaag gcttcatgaa attcaggctg ttgattttgt catcgttgag ctgatgctat 300
 accttgacac acatcccgaat gataccgatgccatcaaaca atacaaccag tatgccggat 360
 tttccagaaa actgaaagcg aagtttgaat caaaatacgg ccctttgatt caaggaagcc 420
 cggatcagac ggaatcctat tggagctgga aaagaagtcc ttggccatgg caagttaa 480
 agaggaaggg agtcaggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct 533
 Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro
 1 5 10
 gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag 581
 Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu
 15 20 25
 caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg 629
 Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu
 30 35 40
 aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac 677

10295.204.ST25.txt

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Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp
 45      50      55
atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta 725
ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val 75
60
tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg 773
Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly 90
ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac 821
Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn 105
gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat 869
Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp 110
ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa ggc agg 917
Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg 125
gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat 965
Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn 140
gac ggc ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc 1013
Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg 160
ttc cgc gaa gct gtc gaa att ttg aag gaa gag cgc gac cgt aaa aaa 1061
Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys 175
gtg ttt taaacagcaa aaagccgaaa atacgaccgt attttcggct ttttatttac 1117
Val Phe
tgcaccgggc tcgcaagcag ttctgctgcg cggtcgcgca gcacatattt ttgaactttt 1177
ccggatgcgg tcagcgggta ttcgtcgatc agaaatacgt actccggaat ttataatac 1237
gaaagctgtc ctttgcaaaa atctctgacg tcttcgagcg tcagcttttt gcccggcctg 1297
catttaataa aggcagccgt tttttccccg tacttttcat ccggaacgcc gacaacctgt 1357
acatcgacaa tatcctcatg ttcataaagg aattcctcta tttcacgcgg gtaaattgtt 1417
tccccgccgc ggacgatcat atcttttaag cgccccggtaa tcctcacgta tccgtccccg 1477
tccatttctg ccaaatctcc ggtatggagc cagccgtctt catcgatggc cttttttgtg 1537
gcttcatcca ttttatagta gcctttcatg acg 1570

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<210> 14
 <211> 189
 <212> PRT
 <213> Bacillus licheniformis

<400> 14

Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro Val Arg Val Arg Glu
 1 5 10 15

Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu Gln Tyr Gly Gly Ala
 Page 17

10295.204.ST25.txt

20

25

30

Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu Asn Gln Arg Tyr Ser
35 40 45

Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp Ile Gly Thr Glu Glu
50 55 60

Phe Ala His Leu Glu Met Ile Ala Thr Met Val Tyr Lys Leu Thr Lys
65 70 75 80

Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr
85 90 95

Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn Ala Ala Gly Val Pro
100 105 110

Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp Pro Ile Ala Asp Leu
115 120 125

Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp
130 135 140

Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn Asp Gly Leu Ala Phe
145 150 155 160

Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg Phe Arg Glu Ala Val
165 170 175

Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys Val Phe
180 185

<210> 15
<211> 1241
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (519)..(1028)

<400> 15
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tgaaaaactt caagagaacg tagatccgat aatgaaatca gttgttaaaa atatcttgaa 120
aaatcgggga gtaaccagcg ataaagtctg gacgctctca gaagaagaaa aagaaaatat 180
tttcaatatg ctggaagatc taaaaaaaca aaccgatgct ttgggttcaaa aacagaaaga 240
aaaagcagcc gcaccgaatg aaaaagggac aaagagagaa aagaacgctg atgcgtcatc 300
agaaaatggc gagagaccaa gaagaagaag aaacagaaca aatagactga gagaaaaact 360
tcgacaacgg agggagcaag aaaacacagc aacagcggaa aattcaaccg agtcagatac 420

10295.204.ST25.txt

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ttcagcagaa aaaaatgggg attttagta gggatatctgt cttatacaag ttaaggagtt 480
acaacatttta ataatagtaa atggaaggag gaaaagaa atg gaa aca aga cca tat 536
                               Met Glu Thr Arg Pro Tyr
                               1                               5

tca tgg att gcg ctt gac ccg gaa tgc gaa cat cca ggc aac gat tat 584
Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu His Pro Gly Asn Asp Tyr
                               10                               20

cac cct agt tat cct aag aaa aaa tta tgt gac gac tat act tgc aac 632
His Pro Ser Tyr Pro Lys Lys Lys Leu Cys Asp Asp Tyr Thr Cys Asn
                               25                               30                               35

tgt ggt agg aaa ggg caa aat ggc ttt atc gat tct gac cta gat caa 680
Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile Asp Ser Asp Leu Asp Gln
                               40                               45                               50

ctt cat ctt aac aaa cag ctc tca gat gaa acg atc atc att aaa gac 728
Leu His Leu Asn Lys Gln Leu Ser Asp Glu Thr Ile Ile Ile Lys Asp
                               55                               60                               65                               70

tct tgt gat gtt caa gtc tca act gaa gac aca caa acg ttg gca tca 776
Ser Cys Asp Val Gln Val Ser Thr Glu Asp Thr Gln Thr Leu Ala Ser
                               75                               80                               85

gtc atg aca gct gca caa aca cta gct gtt act att att ctc gcc att 824
Val Met Thr Ala Ala Gln Thr Leu Ala Val Thr Ile Ile Leu Ala Ile
                               90                               95                               100

atc gat gat cct gat cta gcc gaa ctt gtc aca act gat ctg ttg cag 872
Ile Asp Asp Pro Asp Leu Ala Glu Leu Val Thr Thr Asp Leu Leu Gln
                               105                               110                               115

gta act gcc aat aaa caa acg aac aga caa aaa ttg gtg atc gat aat 920
Val Thr Ala Asn Lys Gln Thr Asn Arg Gln Lys Leu Val Ile Asp Asn
                               120                               125                               130

tcc aga aat gta cat gtc aca acc gaa gat aca gac aca gct atc atc 968
Ser Arg Asn Val His Val Thr Thr Glu Asp Thr Asp Thr Ala Ile Ile
                               135                               140                               145                               150

gta agc aca ttt gtt caa act gtt gta atc acc atc acc gcc ctt atc 1016
Val Ser Thr Phe Val Gln Thr Val Val Ile Thr Ile Thr Ala Leu Ile
                               155                               160                               165

gtc ggc ctt cta taattcaaaa agcagagcca accagctctg cttttcttca 1068
Val Gly Leu Leu

tttttataga cgattacca caccaacaag ggcacgggta catatgttgt taaagactaa 1128
agtcaaatat ccctataaaa aggagctgaa atccatgagc tgcggaaaac accatggccg 1188
gcatgaaaat tgtgtatgcg atgcagtaga acagattata aaagaacagg atg 1241

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<210> 16
 <211> 170
 <212> PRT
 <213> Bacillus licheniformis

<400> 16

Met Glu Thr Arg Pro Tyr Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu
 1 5 10 15

10295.204.ST25.txt

His Pro Gly Asn Asp Tyr His Pro Ser Tyr Pro Lys Lys Lys Leu Cys
 20 25 30

Asp Asp Tyr Thr Cys Asn Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile
 35 40 45

Asp Ser Asp Leu Asp Gln Leu His Leu Asn Lys Gln Leu Ser Asp Glu
 50 55 60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp
 65 70 75 80

Thr Gln Thr Leu Ala Ser Val Met Thr Ala Ala Gln Thr Leu Ala Val
 85 90 95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val
 100 105 110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln
 115 120 125

Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp
 130 135 140

Thr Asp Thr Ala Ile Ile Val Ser Thr Phe Val Gln Thr Val Val Ile
 145 150 155 160

Thr Ile Thr Ala Leu Ile Val Gly Leu Leu
 165 170

<210> 17
 <211> 1516
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1013)

<400> 17
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 tgggagctcc gtacggtatg gggggatacg gacagcagcc tgcaggggga cagatgttta 180
 acagaccgga agatgatgaa gactgattcg gaatgggacg atgatctatc gttccttttt 240
 tattgtggac cgctataaac attttcatgc tatttaacgg gaatgtctat aactgtcaag 300
 ggtaactctt cgcaccccgc acatcctaaa aaagagcgca atgctcaa at tcagcgggtt 360
 tcacgggggg tactaccatt ggacagcaag ctgaaagtgt tttcggggat tttgcttttg 420
 acagcaggtc tatctgcatg cggaacgaac gacgctatag ataattggaaa caatacgcg 480
 ccgacgggat attatctcaa atg atg cag atc gta atg cag ggt ctt gat aat 533

10295.204.ST25.txt

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn
1 5 10

gac ggc cct gtt aca gaa atg ctt gaa aac atg aac ggg aga cac ggt 581
Asp Gly Pro Val Thr Glu Met Leu Glu Asn Met Asn Gly Arg His Gly
15 20 25

gca aca aac gta aac aat cga gcg gga aac ggc aat ccc gtt cca aca 629
Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr
30 35 40

ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg 677
Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu
45 50 55

gtg aat acg gcg gat aca ggc tat gac aga ccg gaa aac cgt aaa atc 725
Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile
60 65 70 75

tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa 773
Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu
80 85 90

agc cag gca gtc gta acg aat gaa acg gtc atc atc gcc gta cgg tct 821
Ser Gln Ala Val Val Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser
95 100 105

gat aaa agg ctg aca aat aac gag aga act caa att aga aaa gca gcc 869
Asp Lys Arg Leu Thr Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala
110 115 120

aaa aca ttt gcc gga gac cgg acc gtt caa gtt gtc gag gac gac ggc 917
Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly
125 130 135

gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg 965
Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg
140 145 150 155

gat cgc gga gac acg acg aat aac aat ttg aac cgc ttg cgg aac caa 1013
Asp Arg Gly Asp Thr Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
160 165 170

taacaagcag ggaattgccg gggattcccc ggcaattttt tataagcgct cggccgattc 1073

ctttacaaaa acggggaaaa ccgtataaag tgtacataga gacgagaatt attttgagg 1133

tagaaagtta tggctggcca ttctaaatgg aaaaatatc agagacgaaa aaatgcccaa 1193

gatgctaaac gcggcaaaat tttcatgaag cttgccaaag aaatatatgt agccgcgaaa 1253

gaaggggggac cagatcccga atctaacgca agtctgcgtc tcgtcatcga taaagccaaa 1313

aatgcaaaca tgccaaatga caacatcgac cgcgccatca aaaaagcttc cggcagccag 1373

gatggaaaaa gctatgagga aattacgtat gagggctacg gaccaagcgg tgtggctgtc 1433

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10295.204.ST25.txt

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 Glu Met Leu Glu Asn Met Asn Gly Arg His Gly Ala Thr Asn Val Asn
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 Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr Gly Asp Gly Thr Tyr
 35 40 45
 Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp
 50 55 60
 Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr
 65 70 75 80
 Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu Ser Gln Ala Val Val
 85 90 95
 Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr
 100 105 110
 Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly
 115 120 125
 Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly Ala Phe Thr Arg Leu
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 145 150 155 160
 Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
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10295.204.ST25.txt

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gtaaaaaagg agtatgaatc atg gac aca aca ttg ggc tac ctc cgt gag tca 533
Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser
1 5 10

ctg tcg aat cac ctt gaa cac ggc ata gga caa aac att tac aga aaa 581
Leu Ser Asn His Leu Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys
15 20 25

atc gtt tcc ggg cga tat gcc aat gag gaa gag ttt gtc gag cac ttg 629
Ile Val Ser Gly Arg Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu
30 35 40

gag gag cgg gaa atg gaa ttt ctg aat caa gtg ctt gaa cat gag atg 677
Glu Glu Arg Glu Met Glu Phe Leu Asn Gln Val Leu Glu His Glu Met
45 50 55

aaa tat gcg ctg aat gaa cag gac cat aaa cgg aca aga gaa tta aac 725
Lys Tyr Ala Leu Asn Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn
60 65 70 75

gaa gtg tat gaa ctg ctg ttt tgaaaggcgg gaatgatcaa tgggtgcaat 776
Glu Val Tyr Glu Leu Leu Phe
80

agagcggaaac ggatacacgt ttgaaccgga atacagcgtg accagacaaa acggtgcat 836

ccatgtatac cggcgcggcc ggtttgtcga ggagattccc tttgagtttc acggggagtt 896

tccagagcat gatttaattg aagagcttgt caatcattat tgttatgaaa ataaaatata 956

aggcttgaag aggctgccga ccgggcggct tttatttttg gatttttata tctataatcc 1016

gcttgcagtt ttttagaacg gcagcagaaa agctgccata aatatgacag ctcatgcatc 1076

gctatttttt cttttcgtcg tagtattgaa cagggatcat ggatccttcc gataccattt 1136

tgttatcttc gatatcatgc ggagacgggt gtccctgcttt ttcaaccggg aatgaatcta 1196

cgttgtgttt ttccgaaaag taagggatct tttctttgac gttttgcaag tac 1249

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<213> Bacillus licheniformis

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Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser Leu Ser Asn His Leu
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20 25 30

Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu Glu Glu Arg Glu Met
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Glu Phe Leu Asn Gln Val Leu Glu His Glu Met Lys Tyr Ala Leu Asn
50 55 60

Leu Phe

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<222> (501) .. (1121)

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		gccggtgtgt	tcacattcat	tcagcaaaaag	ctgatgatgg	cgggaacagc	gcagcaaaat	300										
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				1				5					10					
		gat	gaa	gca	gtg	caa	tcc	ggg	ctt	gaa	cag	ctg	ggc	ctt	cat	gca	gat	581
		Asp	Glu	Ala	Val	Gln	Ser	Gly	Leu	Glu	Gln	Leu	Gly	Leu	His	Ala	Asp	
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		Asp	Val	Glu	Val	Asp	Val	Val	Asp	Glu	Gly	Lys	Lys	Gly	Leu	Phe	Gly	
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		att	ttc	ggt	cat	cgg	tct	gca	gtc	gtg	aac	att	cgg	gaa	aaa	ata	gac	677
		Ile	Phe	Gly	His	Arg	Ser	Ala	Val	Val	Asn	Ile	Arg	Glu	Lys	Ile	Asp	
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		Pro	Val	Lys	Glu	Ala	Lys	Gln	Tyr	Leu	Glu	Asn	Val	Ile	Ser	Asn	Met	
		60					65					70					75	
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		Gly	Ile	Gln	Ala	Gln	Val	Thr	Ala	Glu	Glu	Glu	Ser	Lys	Arg	Val	Val	
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		ttt	cag	ttg	aaa	gga	gac	aaa	aca	gct	ctt	tta	att	gga	aaa	agg	gga	821
		Phe	Gln	Leu	Lys	Gly	Asp	Lys	Thr	Ala	Leu	Leu	Ile	Gly	Lys	Arg	Gly	
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		caa	act	tta	aat	gcc	ctt	gaa	acg	ctg	acg	cag	ctc	gtg	ctc	aat	cgt	869
		Gln	Thr	Leu	Asn	Ala	Leu	Glu	Thr	Leu	Thr	Gln	Leu	Val	Leu	Asn	Arg	
				110					115					120				
		cat	tcc	gac	aga	tat	atc	caa	gcg	gtg	gtt	gac	gcc	gaa	gga	tac	cgc	917

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10295.204.ST25.txt

His Ser Asp Arg Tyr Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg
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 gca aag cgg aag gaa aca ctt gct cag ctg gca ttg aag ctt gct gac 965
 Ala Lys Arg Lys Glu Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp
 140 145 150 155
 cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc 1013
 Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser
 160 165 170
 agt gag cgc aag gtc atc cat gat acg ctt gcg ggc tac tcg cag cat 1061
 Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His
 175 180 185
 atc gaa act tac tct acc ggt gaa gac cat aac cgg cac ctt gtc atc 1109
 Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile
 190 195 200
 tca tat aaa aaa taacatgaaa accgaagttc ccaaaattgg ggcttcggtt 1161
 Ser Tyr Lys Lys
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<210> 22
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 <212> PRT
 <213> Bacillus licheniformis

<400> 22

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Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp Asp Val Glu Val Asp
 20 25 30

Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly Ile Phe Gly His Arg
 35 40 45

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala
 50 55 60

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln
 65 70 75 80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly
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10295.204.ST25.txt
90

85

95

Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly Gln Thr Leu Asn Ala
100 105 110

Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg His Ser Asp Arg Tyr
115 120 125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu
130 135 140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln
145 150 155 160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val
165 170 175

Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His Ile Glu Thr Tyr Ser
180 185 190

Thr Gly Glu Asp His Asn Arg His Leu Val Ile Ser Tyr Lys Lys
195 200 205

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<213> Bacillus licheniformis

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tatagaaata taatgatata ataagagaaa tatgagcgta ctttgaaaaa cattcagaag 420
actataggct tggataatct caatccgctg cgttaccacc ataagttttt tatattgaga 480
tagaaaggca ggtgtgaaag ttg gaa gcg agc acc tta ctg att att gat ttt 533
Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe
1 5 10
gaa ttt aca atg cct gag gga aag tat cac ccg caa aat ttt ttc ccg 581
Glu Phe Thr Met Pro Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro
15 20 25
gaa atc ata gaa gca ggg att gta aag acg gtt cat gat gag gtg gtt 629
Glu Ile Ile Glu Ala Gly Ile Val Lys Thr Val His Asp Glu Val Val

i0295.204.ST25.txt

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agg cgc tgc aaa aat ttt ctc agc atc acg cag gaa cag gtt gac caa Arg Arg Cys Lys Asn Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln 60 65 70 75			725
ggc atc acg ttt aac gcg ctg att gaa aag ctg cgg gag ctt gat cct Gly Ile Thr Phe Asn Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro 80 85 90			773
gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gtg Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val 95 100 105			821
ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly 110 115 120			869
gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys 125 130 135			917
aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly 140 145 150 155			965
acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys 160 165 170			1013
ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys 175 180 185			1061
ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His 190 195 200			1109
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 <212> PRT
 <213> Bacillus licheniformis

10295.204.ST25.txt

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 20 25 30

Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser
 35 40 45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn
 50 55 60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn
 65 70 75 80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val
 85 90 95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys
 100 105 110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu
 115 120 125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu
 130 135 140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His
 145 150 155 160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val
 165 170 175

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Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr
 195 200 205

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10295.204.ST25.txt

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tcc gta ttg ggt gtc gga gct ttg act aca agt att gtc ggt ttt gcc 581
Ser Val Leu Gly Val Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala
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ata gag tgg gga aga tat aag gag ctg ttt ctt tcc ttc gag gta ttg 629
Ile Glu Trp Gly Arg Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu
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gag att ctg tct gtt ctt ttc tgg ttt atc ggg gtt ggc atg atc ttt 677
Glu Ile Leu Ser Val Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe
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agc gtg att gct caa atg gga ttt gtg att ttc tta acg att cac cgc 725
Ser Val Ile Ala Gln Met Gly Phe Val Ile Phe Leu Thr Ile His Arg
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ttt gca ctg gaa att ttc aga tct cat tct ttg tgg aat tcg att cag 773
Phe Ala Leu Glu Ile Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln
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ctg ttt ttg att ata ttt gtc gcg ttt gac ttg gtt tac ttg cgc ttt 821
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ctg ttt ttt gaa aaa gat gga ggc tcc atc att ccg tac att tgg ctg 869
Leu Phe Phe Glu Lys Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu
                        110          115          120

ccg ctc ttt att ttg gcg gta ggc att gcg gcc gct tat gca aag caa 917
Pro Leu Phe Ile Leu Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln
                        125          130          135

aaa cag tcc tct aaa aaa acg ttc gtt tcc gca tta ttt cta atg ttt 965
Lys Gln Ser Ser Lys Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe
                        140          145          150          155

gtt ttt act gtg atg gag tgg ttc ccg gcg tta agg gtc aat gaa gag 1013
Val Phe Thr Val Met Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu
                        160          165          170

gac tgg ctc tat tta atg ctg ctt cct tta tta gcc tgc aac gct ttt 1061
Asp Trp Leu Tyr Leu Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe
                        175          180          185

cag ctt tta atg ctg cca aaa ttt cag gca cgc gct tagaccggct 1107
Gln Leu Met Leu Pro Lys Phe Gln Ala Arg Ala
                        190          195

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10295.204.ST25.txt

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 <213> Bacillus licheniformis

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20 25 30

Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu Glu Ile Leu Ser Val
35 40 45

Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe Ser Val Ile Ala Gln
50 55 60

Met Gly Phe Val Ile Phe Leu Thr Ile His Arg Phe Ala Leu Glu Ile
65 70 75 80

Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln Leu Phe Leu Ile Ile
85 90 95

Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe Leu Phe Phe Glu Lys
100 105 110

Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu Pro Leu Phe Ile Leu
115 120 125

Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln Lys Gln Ser Ser Lys
130 135 140

Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe Val Phe Thr Val Met
145 150 155 160

Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu Asp Trp Leu Tyr Leu
165 170 175

Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe Gln Leu Leu Met Leu
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10295.204.ST25.txt
185

180

190

Pro Lys Phe Gln Ala Arg Ala
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<210> 27
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 <213> Bacillus licheniformis

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 gaagtggccg acatcaacgg cctgactgca caggaagtca tcgatattca cacctcgggt 180
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 gcaggggata tcgtgaaatt tgtcagcgtg acagaagagg agtatcacgc gctgaaggag 480
 gggaaatc ttg agc ata gaa gtg tta aag ccg ggt ctg atg aca acg gtt 530
 Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val
 1 5 10
 caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc 578
 Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser
 15 20 25 30
 ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg 626
 Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly
 35 40 45
 aac agc cag aac gaa gct gcg ctt gaa gtg acg ctg atg ggg ccg ggg 674
 Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly
 50 55 60
 ccg tct ctc cgc ttt caa aaa cct gct ctt ata gcg gtg acg ggc gct 722
 Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala
 65 70 75
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 Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg
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 gga agc cgt gca tat atg gca gtg gcc ggg gga att gat gtg ccg cct 866
 Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro
 115 120 125
 gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt 914
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140

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 acg ccg ttg tcg gaa gcg ctg cac aga aag ctc gca gac gag ggc aaa 1010
 Thr Pro Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys
 160 165 170
 gaa cgg ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt 1058
 Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe
 175 180 185 190
 ctc ccg cta aaa aag aac ccg gtc att cgt gtc atc aaa ggc gat cag 1106
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 195 200 205
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 ttc cgg gtg acg gct aaa tcc gac cgg atg ggg tac cgt ctt caa gga 1202
 Phe Arg Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly
 225 230 235
 gag gcg ctc gaa ctc act cag cct ctg gaa atg atc tct gaa gcg gta 1250
 Glu Ala Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val
 240 245 250
 tca ttc gga acg att caa gtg ccg ccc gac ggc aat ccg atc gtt ctt 1298
 Ser Phe Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu
 255 260 265 270
 ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc 1346
 Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile
 275 280 285
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 Ala Ser Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln
 290 295 300
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 Val Gln Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile
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 Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu
 320 325 330
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 Tyr Met Leu
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 ctctatacag cgatcgggag gcggtcccct ttatatgccg gagcctgtgc gagaagcatt 1959

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1991

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<400> 28

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 35 40 45

Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser
 50 55 60

Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala Asp Phe
 65 70 75 80

Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe
 85 90 95

Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser
 100 105 110

Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met
 115 120 125

Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe Gln Gly
 130 135 140

Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro Thr Pro
 145 150 155 160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg
 165 170 175

Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe Leu Pro
 180 185 190

Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala
 195 200 205

Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg
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Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala
 225 230 235 240

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Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val Ser Phe
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 275 280 285
 Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln
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 ggtcaagtca aggatttgtc agcttatgaa gaaaggctcg tcgtttctcat cagaaagctg 240
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 tttgatgtaa cagaccgtga gtgcatcgcc gaaattcata tcaagtaaag cggtttttta 480
 ggaatagaac ggaggacatt atg ttt gtt gat cag gtg aaa ata tac gta aaa 533
 Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys 10
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 Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr 25
 15 20
 gtg cca aaa gga ggc cct gcc gga ggt gac ggc gga aaa ggc gga gac 629
 Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp 30 35 40

10295.204.ST25.txt

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45						50					55					
tat Tyr	caa Gln	aga Arg	cat His	ttt Phe	aag Lys	gca Ala	gcg Ala	cg Arg	gga Gly	gaa Glu	cac His	ggc Gly	atg Met	tct Ser	aaa Lys	725
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aac Asn	cag Gln	cac His	ggc Gly	cga Arg	aat Asn	gcc Ala	gaa Glu	gac Asp	atg Met	gtt Val	gtg Val	aaa Lys	gtc Val	ccg Pro	ccc Pro	773
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ggc Gly	acg Thr	gtt Val	gtc Val	att Ile	gac Asp	gat Asp	gat Asp	aca Thr	aaa Lys	cag Gln	gtc Val	atc Ile	gct Ala	gat Asp	tta Leu	821
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acg Thr	gag Glu	cac His	gga Gly	cag Gln	gaa Glu	gcc Ala	gtc Val	atc Ile	gca Ala	aaa Lys	ggg Gly	gga Gly	cgc Arg	ggc Gly	gga Gly	869
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cgg Arg	ggc Gly	aat Asn	aca Thr	cgt Arg	ttt Phe	gcg Ala	acg Thr	cct Pro	gcc Ala	aac Asn	ccg Pro	gcg Ala	ccg Pro	cag Gln	ctt Leu	917
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tct Ser	gaa Glu	aac Asn	ggc Gly	gaa Glu	ccc Pro	ggc Gly	aag Lys	gag Glu	cg Arg	tat Tyr	att Ile	gtt Val	ctc Leu	gag Glu	ctg Leu	965
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		190					195					200				
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gcg Ala	cac His	gaa Glu	gga Gly	gtt Val	ggc Gly	ctc Leu	gga Gly	cac His	caa Gln	ttc Phe	ctc Leu	agg Arg	cat His	atc Ile	gaa Glu	1205
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cgc Arg	gac Asp	ccg Pro	tat Tyr	gaa Glu	gat Asp	tat Tyr	gtg Val	acc Thr	att Ile	aat Asn	aaa Lys	gag Glu	ctt Leu	gaa Glu	cag Gln	1301
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tat Tyr	aat Asn	ctc Leu	agg Arg	ctg Leu	aca Thr	gaa Glu	cgt Arg	cct Pro	caa Gln	att Ile	att Ile	gtc Val	gcc Ala	aat Asn	aaa Lys	1349
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atg Met	gat Asp	atg Met	ccg Pro	gat Asp	gcg Ala	gaa Glu	gaa Glu	aat Asn	ctg Leu	aag Lys	gct Ala	ttc Phe	aaa Lys	gaa Glu	aag Lys	1397
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ctc Leu	aca Thr	gat Asp	gat Asp	tat Tyr	cct Pro	gtt Val	ttt Phe	cca Pro	atc Ile	agc Ser	gcg Ala	gtg Val	acc Thr	aga Arg	caa Gln	1445
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 335 340 345

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 350 355 360

cct gac ggc acc ttc gtg ctc agc gga gcc aag ctt gaa cgc tta ttt 1637
 Pro Asp Gly Thr Phe Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe
 365 370 375

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 Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg
 380 385 390 395

cag ctt cgc gga atg ggc gtc gat gat gcg ctt cgg gcc cgc ggt gca 1733
 Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala
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aaa gac ggg gat acg atc cgt ctt ctc gaa ttt gaa ttt gaa ttt atc 1781
 Lys Asp Gly Asp Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile
 415 420 425

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 Asp

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aagtctgtga aagaggagac cttttatctt gtcaggggaag acgtgctgcc ggaggcaatg 1954

cggaaaacac ttgaggtcaa aaagctgatt gagcggaaaa aagcggaaatc tgtagctgaa 2014

gccgtacaaa aggtagatttt gagccgaagc gctttttata agtacagaga tgcggttttt 2074

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 20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
 35 40 45

10295.204.ST25.txt

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
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 Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
 65 70 75 80
 Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
 85 90 95
 Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
 100 105 110
 Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
 115 120 125
 Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
 130 135 140
 Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp
 145 150 155 160
 Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser
 165 170 175
 Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr
 180 185 190
 Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe
 195 200 205
 Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val
 210 215 220
 Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile
 225 230 235 240
 Val His Val Ile Asp Met Ser Gly Leu Glu Gly Arg Asp Pro Tyr Glu
 245 250 255
 Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln Tyr Asn Leu Arg Leu
 260 265 270
 Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys Met Asp Met Pro Asp
 275 280 285
 Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys Leu Thr Asp Asp Tyr
 290 295 300
 Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln Gly Leu Arg Asp Leu
 305 310 315 320

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 340 345 350

Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp Pro Asp Gly Thr Phe
 355 360 365

Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe
 370 375 380

Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg Gln Leu Arg Gly Met
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 Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile 10
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 Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu 25
 15
 gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629
 Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu 40
 30 35

10295.204.ST25.txt

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tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly 80 85 90	773
ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser 95 100 105	821
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys 110 115 120	869
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aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met 140 145 150 155	965
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gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile 175 180 185	1061
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tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu 300 305 310 315	1445

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 335 340 345

gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc 1589
 Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
 350 355 360

aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga 1636
 Lys Arg Gly Asp Phe Leu Tyr Glu Ile
 365 370

cccttgcttt gggcttggtg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac 1696

aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcagggtcat 1756

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 <213> Bacillus licheniformis

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 20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
 35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
 50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
 65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
 85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
 100 105 110

10295.204.ST25.txt

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
 115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
 130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
 145 150 155 160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
 165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
 180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
 195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
 210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
 225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
 245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
 260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
 275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
 290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
 305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
 325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
 340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
 355 360 365

Leu Tyr Glu Ile
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<210> 33
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tatagtaaag cgaatagagg aggggtataca aatgaatcct tactatatga tgctcttatg	240
ttatgtccta tcgatcatcc actttttaat aggctaccgg gaagccctga aaataagcgg	300
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gccacaacaa atgcattttcc gtgttattca cagacggcgg cagtttatgc tatgattaat	480
agaacttcaa tttacaaaaa attcacaaaag attggaggga aaagaatggc caaagccggg	533
cttctcaaga agtcgccaat atg ctg aac gac tgg tac ata ctg atg aaa aaa	581
Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys	
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cga gac att tca ggt tca atc gaa atg aaa gat gac ata gat aaa gca	629
Arg Asp Ile Ser Gly Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala	
15 20 25	
att gaa aag atg gaa gaa gat cat gac gtt ctt ctc tat tat caa atg	677
Ile Glu Lys Met Glu Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met	
30 35 40	
ctg gat ttt cgc tta agg ctt ctt ctt gaa gat atc tcc caa tct tcc	725
Leu Asp Phe Arg Leu Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser	
45 50 55	
aca gaa aaa ttg gaa gcc atc agt ttt aag gac aaa gat cca aaa agt	773
Thr Glu Lys Leu Glu Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser	
60 65 70 75	
acg gac gat aag ctg aat tat tat ttt tat ctg ttc aaa ggg att tat	821
Thr Asp Asp Lys Leu Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr	
80 85 90	
gaa gac tac aag caa aac cat aca gaa gcg ctt aat ttt ttc aga ata	869
Glu Asp Tyr Lys Gln Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile	
95 100 105	
gcg gaa aaa agg ctg agc gtc att caa aat gaa att gaa aaa gcc gaa	917
Ala Glu Lys Arg Leu Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Thr Trp	
110 115 120	
ttt cat tat aaa atc ggt gtt ttg tat tac aac tta aaa gcg aca tgg	965
Phe His Tyr Lys Ile Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp	
125 130 135	
ctg tcg att cac cac atc aac att gcc tca ggc atc ttc caa ggg tat	1013
Leu Ser Ile His His Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr	
140 145 150 155	
gac ggg tat gcc aag cgg gtc atc aac tgc aaa atg ctg atc ggg ctc	
Page 42	

10295.204.ST25.txt

Asp Gly Tyr Ala Lys Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu
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 aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag 1061
 Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys
 175 180 185
 gaa gca att gaa aaa acc gaa aaa atc gcc gac caa tat ctt ttg cct 1109
 Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro
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 tat acc tac tat aat atg gcc ttt ttg aag agt aag gaa gat aaa cac 1157
 Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His
 205 210 215
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 Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe
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 240 245 250
 agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc 1301
 Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile
 255 260 265
 gac aca gcc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa 1349
 Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu
 270 275 280
 tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa 1397
 Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys
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 ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca 1445
 Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala
 300 305 310 315
 tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg 1493
 Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg
 320 325 330
 gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac 1541
 Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp
 335 340 345
 aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt 1594
 Lys Ala Ser Lys Leu Ala Gly Arg Gly Gly Glu
 350 355
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10295.204.ST25.txt

<210> 34
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 <213> Bacillus licheniformis

<400> 34

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 35 40 45
 Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu
 50 55 60
 Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu
 65 70 75 80
 Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln
 85 90 95
 Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu
 100 105 110
 Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile
 115 120 125
 Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His
 130 135 140
 Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys
 145 150 155 160
 Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln
 165 170 175
 Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys
 180 185 190
 Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn
 195 200 205
 Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys
 210 215 220
 Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys
 225 230 235 240

10295.204.ST25.txt

Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys
245 250 255

Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys
260 265 270

Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr
275 280 285

Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys
290 295 300

Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu
305 310 315 320

Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr
325 330 335

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Ala Gly Arg Gly Gly Glu
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<212> DNA
<213> Bacillus licheniformis

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ggaaaagtgc tcccggggca gacatcctgt tatacaccga tggttgattt cgatccgcgt 180
tcttcatatg cgatgtagaa acattatcaa tccattaaca ggagctctca cttattccta 240
tacaagttcg tattcatatt tgaagaagta gtgtataaaa gcaccctttc agcaaggggtg 300
ctttttgctg tcttatcagt cacggtttca cagctattga agagtcattt gacctaataa 360
aagagtggga aaagtggggg attcaggaaa ctgtgtataaaa tgaactatta ctattaattt 420
atacaggggag gaaaatatag tatgatatga ataatgaata aaatacaaaa aaattgaata 480
tcggaagaaa ggagctccat atg aac aag atc gcc gcg gaa gaa gtc gcc aac 533
Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn
1 5 10
atc ctt aat aca tgg tac cgc gcc atc aga aga aat gat gct gaa cag 581
Ile Leu Asn Thr Trp Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln
15 20 25

10295.204.ST25.txt

tcg atc cga ata ttt gaa gaa gtc aaa ccg atg ctg gca gag atg gag Ser Ile Arg Ile Phe Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu 30 35 40	629
gaa gac caa gag gtt tta atc tac tat tct ctg ctg gaa ctg cgg cat Glu Asp Gln Glu Val Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His 45 50 55	677
aaa atc atg ctg tat gat acg cgg gga aaa aag ata gaa cag caa gag Lys Ile Met Leu Tyr Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu 60 65 70 75	725
gag tta acg aac ggc ggc agt gct gca tca cat atg aca tcc tat tac Glu Leu Thr Asn Gly Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr 80 85 90	773
tac tac ctg ttt tca gga gct tat gaa gtg tat aaa aag aat tat gag Tyr Tyr Leu Phe Ser Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu 95 100 105	821
cag gcg atc agc ttc tat aaa att gcc gag aag aag ctt gct cat gta Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val 110 115 120	869
cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu 125 130 135	917
tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cgg cag Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln 140 145 150 155	965
gcg atg gaa att ttc aag ggg cat gcc gac cat gat atg aac ctt gtt Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val 160 165 170	1013
tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Thr Glu Met Gly Lys Tyr 175 180 185	1061
aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys 190 195 200	1109
gcc gcc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu 205 210 215	1157
ctt tat gcg gcg atg gac aat tcg gaa aaa agc att cag ttt tta gaa Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu 220 225 230 235	1205
atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn 240 245 250	1253
gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys 255 260 265	1301
cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc gcg Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala 270 275 280	1349
gcg aat aaa ata ttt gac gcc aaa atc gat att tta tat gcg gct tat Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr 285 290 295	1397

10295.204.ST25.txt

gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa 1445
 Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu 315
 300 305 310
 atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc 1493
 Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu 330
 320 325
 tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca 1541
 Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala 345
 335 340
 cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg 1589
 His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val 360
 350 355
 gag gga atg tgatgaaaaa actgttcatt gttgctgcga ttgctgccgt 1638
 Glu Gly Met 365
 cgtatgttcg ggatggtttg cggcagaaac tcaactgggca tccggcgaca tgcaggttgc 1698
 tgaaaagatg gtcggttaaa tcgaatactc ggaacaaata tgaacatccg ctcctgagca 1758
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<210> 36
 <211> 366
 <212> PRT
 <213> Bacillus licheniformis

<400> 36

Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp
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Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe
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Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val
35 40 45

Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr
50 55 60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly
65 70 75 80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser
85 90 95

10295.204.ST25.txt

Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu Gln Ala Ile Ser Phe
 100 105 110

Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val His Asp Glu Ile Glu
 115 120 125

Val Ala Gln Phe His Asp Lys Val Gly Lys Leu Tyr Tyr Tyr Leu Gly
 130 135 140

Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln Ala Met Glu Ile Phe
 145 150 155 160

Lys Gly His Gly Asp His Asp Met Asn Leu Val Ser Thr Tyr Ile Thr
 165 170 175

Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr Thr Glu Ala Glu Glu
 180 185 190

Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys Ala Gly Asp Cys Phe
 195 200 205

Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu Leu Tyr Ala Ala Met
 210 215 220

Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu Ile Val Leu Asp Asp
 225 230 235 240

Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn Ala Val Phe Leu Met
 245 250 255

Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys Arg Ala Ala Ala Phe
 260 265 270

Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala Ala Asn Lys Ile Phe
 275 280 285

Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr Ala Gly Asp Gly Glu
 290 295 300

Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu Ile Leu Phe Gln Thr
 305 310 315 320

Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val
 325 330 335

Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu
 340 345 350

Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met
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<210> 37
<211> 1936
<212> DNA
<213> Bacillus licheniformis
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10295.204.ST25.txt

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Val Ala Ala Ala Gly Tyr His His Pro Tyr Pro Tyr Pro Phe Tyr
190 200

1037
cct gga ggc tgc tgg att cct gtt tca ccg gtg ctg cct gga tcg gga
Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly
205 210 215

1085
ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat
Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His
220 225 230

1133
cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg
Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met
235 240 245 250

1181
ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act
Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr
255 260 265

1229
gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca
Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro
270 275 280

1277
aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat
Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp
285 290 295

1325
gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg
Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala
300 305 310

1373
gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg
Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly
315 320 325 330

1421
gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa
Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu
335 340 345

1473
gat gat gaa gac tgattcgga tgggacgatg atctatcggt ccttttttat
Asp Asp Glu Asp
350

1533
tgtggaccgc tataaacatt ttcattgctat ttaacgggaa tgtctataac tgtcaagggt

1593
aactcttcgc atcccgacaca tcctaaaaaa gagcgcaatg ctcaaattca gcggttttca

1653
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1713
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1773
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1833
ttacagaaat gcttgaaaac atgaacggga gacacggtgc aacaaacgta aacaatcgag

1893
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1936
atcacaacca tttggtgaat acggcggata caggctatga cag

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<211> 350
<212> PRT
<213> Bacillus licheniformis

10295.204.ST25.txt

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 35 40 45
 Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys
 50 55 60
 Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro
 65 70 75 80
 Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser
 85 90 95
 Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro
 100 105 110
 Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln
 115 120 125
 Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn
 130 135 140
 Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val
 145 150 155 160
 Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp
 165 170 175
 Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr
 180 185 190
 His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile
 195 200 205
 Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr
 210 215 220
 Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser
 225 230 235 240
 Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly
 245 250 255
 His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro

10295.204.ST25.txt
265

270

260

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly
275 280 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro
290 295 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met
305 310 315 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro
325 330 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp
340 345 350

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<211> 2027
<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (501)..(1526)

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ttgtttatct gaatgatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa 180
gggggattct gatatgccta ggcagccatt caaactggga gatgagggtgt atgtcattta 240
ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtcg ttgatcatcc 300
gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct ttgccgaaga 360
tgatgccgtt ttttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg 420
gatatgaaga cattaccggt atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc 480
aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat 533
Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr 10
1
att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat 581
Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp 25
15
aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac 629
Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn 40
30
cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat 677
Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn 55
45
gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat 725
Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp

10295.204.ST25.txt

60	65	70	75	
tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt	Ser Ser Lys Pro Ser 80	Ala Glu Tyr Ala Ile 85	Pro Phe Ala Thr Gly Cys 90	773
atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag	Met Gly His Cys 95	His Tyr Cys Tyr Leu 100	Gln Thr Thr Met Gly Ser Lys 105	821
ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg	Pro Tyr Ile Arg Thr Tyr Val Asn 115	Val Glu Glu Ile Leu 120	Glu Gln Ala	869
gat caa tat ata aaa gaa agg gct ccc gaa gat acg cgg ttt gaa gct	Asp Gln Tyr Ile Lys Glu Arg 130	Ala Pro Glu Asp Thr 135	Arg Phe Glu Ala	917
tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta	Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu 155			965
aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt	Lys Arg Ala Ile Glu His Phe Gly Gln Thr 165	Asp His Gly Lys Leu Arg 170		1013
ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac	Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His 185			1061
aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att	Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile 200			1109
aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cgg atc gaa gcc	Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala 215			1157
gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttt atc atc gct	Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala 235			1205
ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg	Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu 250			1253
gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc	Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr 265			1301
ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att	Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile 280			1349
gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cgg	Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg 295			1397
cgc tat aaa tgg ggc aga tac ggg att ggc aaa tac att tat cag aag	Arg Tyr Lys Trp Gly Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys 315			1445
gat gaa gaa gca gag ctt cgc agc gcc ctt gaa tcg tat atc gac aac	Asp Glu Glu Ala Glu Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn 330			1493
tat ttt ccc gaa gca aaa atc gaa tat ttc aca taacagagct ttagttgata	Tyr Phe Pro Glu Ala Lys Ile Glu Tyr Phe Thr			1546

10295.204.ST25.txt
340

335

aagctctgtt ttttgtttt aaaacattat gttaaaaaag gatttttcca ctccattaac 1606
 accgcataat caagcgattc ctcatcttca atgtagccgg gaatcacaca aactggagag 1666
 cgtccgcaat gaagcaggaa cgagagcact ggatcgcgct tttccccgtc caatacagct 1726
 tgaacatact gttcgggctt catttcttca gccgacttgt gataatgggg aatccgtccg 1786
 ccgccaatga gacgcttgag ccctttaaag accgtcagtt catacatgga ttgcatcagc 1846
 cgcattccga tgccgagttt tcgatagtcg ggggacacgg aaatatcgac gacataaagg 1906
 gagtttccat cgttttgatg tgtgccgata taccggttgt ccgtcacttc atcccagctg 1966
 tggtgcggat gatgcggatc aaaatcagcc atgagcgctg tcatcgaacc gatgatgcgg 2026
 c 2027

<210> 40
 <211> 342
 <212> PRT
 <213> Bacillus licheniformis

<400> 40

Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr Ile Glu Pro Arg Ala
1 5 10 15

Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp Lys Phe Ser Asn Met
20 25 30

Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn Gln Val Arg Asn Ile
35 40 45

Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn Ala Lys Ser Thr Leu
50 55 60

Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp Ser Ser Lys Pro Ser
65 70 75 80

Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys Met Gly His Cys His
85 90 95

Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys Pro Tyr Ile Arg Thr
100 105 110

Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala Asp Gln Tyr Ile Lys
115 120 125

Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala Ser Cys Thr Ser Asp
130 135 140

Ile Val Gly Ile Asp His Leu Thr His Thr Leu Lys Arg Ala Ile Glu
145 150 155 160

10295.204.ST25.txt

His Phe Gly Gln Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe
 165 170 175

His His Val Asp His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg
 180 185 190

Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro
 195 200 205

Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala
 210 215 220

Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His
 225 230 235 240

Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg
 245 250 255

Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln
 260 265 270

His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro
 275 280 285

Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly
 290 295 300

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu
 305 310 315 320

Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn Tyr Phe Pro Glu Ala
 325 330 335

Lys Ile Glu Tyr Phe Thr
 340

<210> 41
 <211> 905
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(905)

<400> 41
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 tccatttcat cgaaagacgg aaccgatttg atcgccgtca caatcaatgc ccctgacgac 120
 tggaatgatc atatgaacat gttcaactat gtattcggcc agtacaaaac atatatcatc 180
 gccaaaaaag gcgagattcc gaaattaaaa gactcttttt acggacatac agctttttatt 240
 aaacgggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa gggtgatatc 300

gagcttcttg aaccgaaaaa atcatggcgt aaaaacaaaa aagaaatccc ggacatcatc	360
ggagaaatga acgtcatgtt cgacggaaaa acgattgcaa gcgtaccgat ctattatgaa	420
aacgagcgaa acaaaaaatcc gaaaaaatcg tttttcgaga cttttcaatc cgtattccaa	480
aaagcggcgg gcggttcatc atg gtc aat ata atc tgg gtc ggc tta acg gtg Met Val Asn Ile Ile Trp Val Gly Leu Thr Val 1 5 10	533
atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn 15 20 25	581
gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly 30 35 40	629
ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu 45 50 55	677
cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile 60 65 70 75	725
tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr 80 85 90	773
att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala 95 100 105	821
aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac ccg Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg 110 115 120	869
aac cgc agg gaa gcg agc cgc tca atg cac cca ggc Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly 125 130 135	905

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<210> 42
<211> 135
<212> PRT
<213> Bacillus licheniformis
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<400> 42

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<400> 42
Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe
1          5          10          15

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Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys
20 25 30

Gly ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu
35 40 45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu
50 55 60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro

10295.204.ST25.txt

65

70

75

80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu
85 90 95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile
100 105 110

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala
115 120 125

Ser Arg Ser Met His Pro Gly
130 135

<210> 43
<211> 1568
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1076)

<220>
<221> CDS
<222> (1112)..(1567)

<400> 43
gattagatct tcagtttttt gcatctaaaa aaggagtagg ttcaacgaaa aacggacgtg 60
actctgaagc gaagcgccta ggtgctaaac gtgcagacgg tcaattcgta tctggccgtt 120
caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc 180
gatattacac tctatttgca aaagtcgacg gaactgttaa attcgaacct ttcggccgta 240
cccccaaaaa agtgagcgta tatcctgtag cctaaccttt aaacgaaact cgggtcgttc 300
tgaccggagt tttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa 360
ataaggccgg gtttccgctc tgattctgct tcgttaaagt atataaacgt gtttcattta 420
tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc 480
aaacgattgg gagtgcctaa atg gaa gaa act tcg aaa aaa cga gaa aag aat 533
Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn
1 5 10
atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac 581
Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His
15 20 25
tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta 629
Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu
30 35 40
aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc 677
Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val
45 50 55
atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc 725
Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg

10295.204.ST25.txt

60	65	70	75	
gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp 85 Met Ala His Ser Leu Thr				773
ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu				821
gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp				869
gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr				917
gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val				965
ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp				1013
ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala				1061
gaa att cat atc aag taaagcgggtt ttttaggaat agaacggagg acatt atg Glu Ile His Ile Lys Met				1114
ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn				1162
ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro				1210
gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val Asp				1258
gaa ggt ctc agc acg ctg atg gat ttt aga tat caa aga cat ttt aag Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys				1306
gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn				1354
gcc gaa gac atg gtt gtg aaa gtc ccg ccc ggc acg gtt gtc att gac Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp				1402
gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu				1450
gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg Phe				1498
gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro				1546

10295.204.ST25.txt
330

325

335

1568

ggc aag gag cgc tat att gtt c
 Gly Lys Glu Arg Tyr Ile Val
 340

<210> 44
 <211> 192
 <212> PRT
 <213> Bacillus licheniformis
 <400> 44

Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn Met Asp Asp Lys Ala
 1 5 10 15

Leu Thr His Glu Leu Ile His Leu Leu Ser His Ser Arg His Asp Trp
 20 25 30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr
 35 40 45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His
 50 55 60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu
 65 70 75 80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val
 85 90 95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val
 100 105 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly
 115 120 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp
 130 135 140

Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr
 145 150 155 160

Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys
 165 170 175

Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys
 180 185 190

<210> 45
 <211> 152
 <212> PRT
 <213> Bacillus licheniformis
 <400> 45

10295.204.ST25.txt

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
1 5 10 15

Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
35 40 45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
50 55 60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65 70 75 80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
85 90 95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
100 105 110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
115 120 125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
130 135 140

Pro Gly Lys Glu Arg Tyr Ile Val
145 150

<210> 46
<211> 1849
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1346)

<400> 46
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agtccggctg aaaagggctt tggaatcggt caaacaaaac tatgatttca tgattattga 120
ctgcccgcg tcataggggc tgcttacaat caatgcgctt acggcttccg attccgctcg 180
gattccgggtc cagtgcgagt attatgcgct ggaagggctg agccagctgc tcaactctgt 240
ccggctcgtg caaaaacatt taaatacggg tctgatgatc gacggcgat tgctgacaat 300
gcttgatgca agaacgaatt taggcataca ggtcatcgaa gaagtgaata agtacttccg 360
cgataaagta tacaaaacgg ttatcccccg gaatgtccgg ctcaagtgaag cgccgagtca 420
tggaagccg atcattttat atgatccccg ttccagagga gcggaagtct atttagaatt 480

10295.204.ST25.txt

agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca 533
Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala
1 5 10

ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag 581
Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys
15 20 25

ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat 629
Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp
30 35 40

gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt 677
Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val
45 50 55

ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtt 725
Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val
60 65 70 75

gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc 773
Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr
80 85 90

att cct gcg att gtg cgc gag ctg tcg gaa tcc ctg atg atg gag att 821
Ile Pro Ala Ile Val Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile
95 100 105

gcc cta ttg gaa aat ctt caa cga gaa gac ctg tct ccg ctt gaa gaa 869
Ala Leu Leu Glu Asn Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu
110 115 120

gca aaa gcc tat gaa tct ttg ctc aaa cat ctc gat atg acc cag gaa 917
Ala Lys Ala Tyr Glu Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu
125 130 135

cag ctg gcg aaa agg ctt gga aaa agc agg cct cac atc gcc aac cac 965
Gln Leu Ala Lys Arg Leu Gly Lys Ser Arg Pro His Ile Ala Asn His
140 145 150 155

ttg cgg ctg ctg aca ctt cct gaa gac gtt caa aag tta atc gac aac 1013
Leu Arg Leu Leu Thr Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn
160 165 170

ggc acg tta tcg atg ggc cat ggc cga aca ttg ctt gga ttg aaa aac 1061
Gly Thr Leu Ser Met Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn
175 180 185

aag aaa aag ctt gag ccg ctt gtt caa aag gtc gtg tcc gaa cag ttg 1109
Lys Lys Lys Leu Glu Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu
190 195 200

aac gtc cgc cag ttg gaa aag tta att caa cag ttg aac gct gat gtt 1157
Asn Val Arg Gln Leu Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val
205 210 215

cca cgt gaa aca aag aag ccg aaa caa gtc aaa gat gca gtg atc aag 1205
Pro Arg Glu Thr Lys Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys
220 225 230 235

gaa cgg gaa tcg tat ttg cga aac tat ttt gga aca ccg gtg acc att 1253
Glu Arg Glu Ser Tyr Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile
240 245 250

aaa aag caa aag aaa aaa ggc agg atc gaa atc gaa ttc tac tca aat 1301
Lys Lys Gln Lys Lys Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn
255 260 265

10295.204.ST25.txt

gaa gac ttg gag cgt att ctc gaa tta ttg gct caa gaa gac gca 1346
 Glu Asp Leu Glu Arg Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
 270 275 280

taagcttaaa aaccatctga tcatgtacag atgggttttt tatgacattc ttccggtcat 1406
 tctttcaatt ggtgacacat ggcgccgctg cgatccggtc ttttccagat gcgacagccc 1466
 gtccgcaagc acatttgcca tgctcatgac aagattgagc cttgtatttt gcaggacaaa 1526
 atactccata aaaccgctga cattgacaat tccgttaata tgcacgtggc cgacttccgg 1586
 caaactttttc tgaacgcctg ctcccggctt caaaggccct ttgccgattt ggaaagaccc 1646
 cacgctttttg gttcgtccaa gacaggcgctc gatcgcgatc ataaaaggat tttgatgctg 1706
 ctgatgaata tgatcaagct tttcatttaa gttcacggcg tgaaccgggt cggcaagcgt 1766
 tccatagaca tgaaaacgtg tcagctgctt tgcggagagt ttcattccta cgaggggacc 1826
 gagcgaatct ccggtcgagc ggt 1849

<210> 47
 <211> 282
 <212> PRT
 <213> Bacillus licheniformis

<400> 47

Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala Leu Phe Ser Asn Val
 1 5 10 15

Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys Leu Gln Asp Leu Arg
 20 25 30

Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp Asp Gln Ser Leu Lys
 35 40 45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile
 50 55 60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg
 65 70 75 80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val
 85 90 95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn
 100 105 110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu
 115 120 125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg
 130 135 140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr
 145 150 155 160

10295.204.ST25.txt

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met
 165 170 175

Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu
 180 185 190

Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu
 195 200 205

Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys
 210 215 220

Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr
 225 230 235 240

Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile Lys Lys Gln Lys Lys
 245 250 255

Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg
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Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
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 agaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacgggtc ataccctga 180
 ggtcgggggt tcgatccctt ccgccgctac ttatatgaag gcccgttggt caagtggta 240
 agacaccgcc ctttcacggc ggtaacacgg gttcgaatcc cgtacgggtc attccggaaa 300
 ccggcttctt ctgaagccgg ttttttgctg cataaaaata tgcaaaataa cgggaatgga 360
 ctcgacttat caagagtgat tgaagcatgc tacaaaaagc gtcgaacagt tctttgaatt 420
 cgttaccttc ttttgacaaa atcctatttc atctttcgct ataattggcaa gcaacgaata 480
 aacgagtggg agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca 533
 Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro
 1 5 10
 ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg 581
 Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met
 15 20 25

10295.204.ST25.txt

acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly 30 35 40	629
ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu 45 50 55	677
tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu 60 65 70 75	725
atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly 80 85 90	773
gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu 95 100 105	821
ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp 110 115 120	869
cggt gtc aga acg ctg cct gtc gtc gtc ttt ttg gcg atg gct gtg aca Arg Val Arg Thr Leu Pro Val Val Phe Leu Ala Met Ala Val Thr 125 130 135	917
aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His 140 145 150 155	965
tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu 160 165 170	1013
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tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc Ser Leu Lys Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser 190 195 200	1109
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ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly 220 225 230 235	1205
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ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala 270 275 280	1349
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ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr 320 325 330	1493
ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg Ile Pro Gly Thr Thr Glu His Ala Gln Glu Gln Gln Tyr Ala Arg 335 340 345	1541
aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val 350 355 360	1589
ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro 365 370 375	1637
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aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val 400 405 410	1733
cag aac ttt gat aaa aca tat gat ttg atg aaa cgg gtt atg cag gaa Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu 415 420 425	1781
acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe 430 435 440	1829
cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac His Gln His Cys Ser Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp 445 450 455	1877
gag ctg act cat ttt agg gcg aac cag aca tta aaa caa aag gtg cat Glu Leu Thr His Phe Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His 460 465 470 475	1925
gac agc aga cgt ctc gtt gca gag cag ctt ctc ggc gtt tct cag gtt Asp Ser Arg Arg Leu Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val 480 485 490	1973
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gaa atg agt atc ccg tat tgc aac ggc cat gga gag tgt gaa aaa atc Glu Met Ser Ile Pro Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile 540 545 550 555	2165
atc gct ccg atg ctg tcc gat att ttg gaa gaa caa att atc gtc aaa Ile Ala Pro Met Leu Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys 560 565 570	2213

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gca gaa cag tgc gcc. ggc cat ccg aat gga tat tgt cat gtt gcc ttc 2261
 Ala Glu Gln Cys Ala Gly His Pro Asn Gly Tyr Cys His Val Ala Phe
 575 580 585

ggt tgc gcg aag tca tac agg gtg gtg aca gga gcc gcg cat gca gca 2309
 Gly Ser Ala Lys Ser Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala
 590 595 600

aaa ggc gga ggg ctt gtc tcc ggc gac agc tac aat atg atg gag ctc 2357
 Lys Gly Gly Gly Leu Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu
 605 610 615

ggc acc ggc aaa tat gcc gcc gcc att agc gat ggt atg gga aat ggc 2405
 Gly Thr Gly Lys Tyr Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly
 620 625 630 635

gca agg gcc cat ttt gaa agc aat gag acg atc aag ctg ctg gaa aag 2453
 Ala Arg Ala His Phe Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys
 640 645 650

att ctt cag tgc ggc atc gac gaa aaa gtg gcg att aaa acg att aac 2501
 Ile Leu Gln Ser Gly Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn
 655 660 665

agc att ctt tca tta agg aca aca gat gaa att tat tgc aca ttg gat 2549
 Ser Ile Leu Ser Leu Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp
 670 675 680

tta tgc gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc 2597
 Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile
 685 690 695

ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg 2645
 Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val
 700 705 710 715

cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat 2693
 Gln Ala Ser Asn Leu Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp
 720 725 730

gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc 2741
 Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser
 735 740 745

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 Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp
 750 755 760

atg aag cgc aaa ttg aaa tgc ctg aaa acc gag gag ccg cag gaa atc 2837
 Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile
 765 770 775

gcc gac tta atc atg gaa gaa gtg atc cgg aca agg tgc ggt ctg att 2885
 Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile
 780 785 790 795

gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca 2933
 Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro
 800 805 810

aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag 2981
 Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu
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 Ile Ser

10295.204.ST25.txt

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Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val
 35 40 45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro
 50 55 60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys
 65 70 75 80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser
 85 90 95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile
 100 105 110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu
 115 120 125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val
 130 135 140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe
 145 150 155 160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser
 165 170 175

10295.204.ST25.txt

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu
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 Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu
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 Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg
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 Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys
 225 230 235 240
 Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly
 245 250 255
 Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly
 260 265 270
 Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile
 275 280 285
 Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val
 290 295 300
 Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr
 305 310 315 320
 Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr
 325 330 335
 Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val
 340 345 350
 Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser
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 Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys
 370 375 380
 Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys
 385 390 395 400
 Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys
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 Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln
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 Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser
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10295.204.ST25.txt

Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe
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Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu
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Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser
 485 490 495

Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln
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Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu
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Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro
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Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu
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Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala
 565 570 575

Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser
 580 585 590

Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Gly Leu
 595 600 605

Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr
 610 615 620

Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe
 625 630 635 640

Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly
 645 650 655

Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu
 660 665 670

Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp
 675 680 685

Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser
 690 695 700

Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu
 705 710 715 720

10295.204.ST25.txt

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln
725 730 735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu
740 745 750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu
755 760 765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met
770 775 780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr
785 790 795 800

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile
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820 825

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Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu
1 5 10

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Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu
15 20 25

aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg 629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala
30 35 40

10295.204.ST25.txt

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cat	cct	gcc	ggc	aaa	ctg	tcg	ttt	tcg	gtt	gtg	atc	gtt	ctt	gtg	gca	725
His	Pro	Ala	Gly	Lys	Leu	Ser	Phe	Ser	Val	Val	Ile	Val	Leu	Val	Ala	
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Phe	Gly	Phe	Lys	Arg	Phe	Arg	Phe	Phe	Leu	Gln	Asn	Leu	Phe	Ser	Phe	
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Tyr	Phe	Ala	Thr	Phe	Leu	Met	Gly	Gly	Gly	Ile	Ile	Gly	Ala	His	Ser	
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Phe	Ala	Ala	Val	Trp	Leu	Phe	Ser	Lys	Lys	Arg	Phe	Glu	Asp	Ala	Glu	
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Ala	Lys	Lys	Ile	Gln	Tyr	Glu	Glu	Arg	Val	Arg	Leu	Glu	Ala	Cys	Ile	
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ggt	gaa	cat	acg	ctt	cat	ttc	acc	gga	ttg	att	gac	tcc	gga	aac	cag	1061
Gly	Glu	His	Thr	Leu	His	Phe	Thr	Gly	Leu	Ile	Asp	Ser	Gly	Asn	Gln	
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Lys	Leu	Lys	Val	Val	Leu	Gly	Glu	Glu	Ala	Ser	Val	Thr	Ile	Lys	Glu	
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Met	Ser	Pro	Leu	Asp	Ala	Val	Gly	Lys	Leu	Asp	Glu	Ala	Leu	Pro	Tyr	
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Ile	Gly	Arg	Ile	Arg	Leu	Ile	Pro	Tyr	Arg	Gly	Val	Gly	His	Gln	His	
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Gln	Phe	Leu	Leu	Cys	Leu	Lys	Pro	Asp	His	Val	Leu	Val	Cys	Thr	Glu	
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Arg	Glu	Val	Ile	Glu	Ala	Pro	Lys	Cys	Leu	Ile	Gly	Ile	Ser	Thr	Ser	
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Pro	Leu	Ser	Ala	Asp	Gly	Glu	Phe	Asp	Ala	Ile	Val	His	Pro	Lys	Met	
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10295.204.ST25.txt
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9

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<400> 51

Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu Asn Phe Cys Phe Asp
 1 5 10 15

Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu Lys Arg Arg Val Lys
 20 25 30

Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu
 35 40 45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys
 50 55 60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg
 65 70 75 80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe
 85 90 95

Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp
 100 105 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly
 115 120 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp
 130 135 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln
 145 150 155 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu
 165 170 175

10295.204.ST25.txt

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile
 180 185 190

Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val
 195 200 205

Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp
 210 215 220

Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg
 225 230 235 240

Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys
 245 250 255

Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu
 260 265 270

Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp
 275 280 285

Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro
 290 295 300

Val Lys His Val Ser
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<210> 52
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 <212> DNA
 <213> Bacillus licheniformis

<220>
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 taagatcatg aagcttttct ttggacaagt caatccgacg gttttgacaa tggcggcggt 180
 aagggtggtg tcatctttga tcgaactgac ggcggctgtt gtgatgcttt tgacaaacga 240
 cgtcagaaaa gctgtggcgg tcaacagcgt actggccatg gtcgggccgc tcatctttat 300
 tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat 360
 tttgatcttt atgggagtggt ttttgatcat cgcggggagc tataaatagc gacacatgat 420
 aagagaggcc gacttgtcat aatgtcttcc tttgatcata catttttata gaagacaagc 480
 aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg 533
 Leu His His Ile Thr Glu Ile Leu Pro Asp Thr
 1 5 10

10295.204.ST25.txt

atc aaa cgc gcg ctc agc ggt ctt ggc gac cat gaa atc gat cag ata Ile Lys Arg Ala Leu Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile 15 20 25	581
gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys 30 35 40	629
gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala 45 50 55	677
ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu 60 65 70 75	725
gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly 80 85 90	773
ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga Leu Ala Gly Arg Val Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg 95 100 105	821
gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile 110 115 120	869
tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr 125 130 135	917
ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp 140 145 150 155	965
ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys 160 165 170	1013
gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly 175 180 185	1061
ata ccg caa tat cgg ctc ggc gac ccg gca gac atc ctt gac gcc tgt Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys 190 195 200	1109
cca aaa gcg gaa ggg ctg atg atg atg atc aga tcg atg agt ccg gag Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu 205 210 215	1157
gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu 220 225 230 235	1205
ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly 240 245 250	1253
tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln 255 260 265	1301
gag cac ccg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly 270 275 280	1349

10295.204.ST25.txt

ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg 1397
 Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly
 285 290 295
 gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttatttttg 1451
 Ala Ala Lys Arg Met Leu Ser Cys
 300 305
 cagcagccac atggacagga tttgaaatgg cgaagccttt cagggaaagg ccgaagcaaa 1511
 tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac 1571
 cgctccgtca ggcatacaaaa cagatcgac accagcttac cgagccggta gcctctttgt 1631
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<210> 53
 <211> 307
 <212> PRT
 <213> Bacillus licheniformis

<400> 53

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 20 25 30

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe
 35 40 45

Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala Leu Leu Leu Asn Arg
 50 55 60

Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu Glu Leu Lys Lys Gly
 65 70 75 80

Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly Leu Ala Gly Arg Val
 85 90 95

Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe
 100 105 110

Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val
 115 120 125

Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro
 130 135 140

10295.204.ST25.txt

Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile
 145 150 155 160
 Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp
 165 170 175
 Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg
 180 185 190
 Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly
 195 200 205
 Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp
 210 215 220
 Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His
 225 230 235 240
 Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp
 245 250 255
 Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe
 260 265 270
 Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser
 275 280 285
 Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met
 290 295 300
 Leu Ser Cys
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<210> 54
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 <212> DNA
 <213> Bacillus licheniformis

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<220>
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 <222> (1036)..(1239)

<220>
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 <222> (1255)..(1509)

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 agttcgggaa gcggcaacgc ccctgccaaa aaagtgggga ttgttgacga aaggtctgaa 120

10295.204.ST25.txt																				180
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gacgcctgtc	caaaag	cgg	agggtgatg	atgatgatca	gatcgatgag	tccggaggta														300
atgatcgccg	atgagatcgg	gagaatggaa	gacgcagaag	cgctcttgga	agcgggtccac															360
gcgggggtga	ctgtcatcgt	ttcggctcac	ggctacacat	atgcagatct	cgccaggcgt															420
ccatcattga	aaatgcttca	agagcaccgg	gtttttgagc	gaatcgtgga	actttccaga															480
aagaacggtc	ccggcagcct	gagccgc	atc	ctaaatggga	acggagagcc	gctcggggca														530
gcaaagagga	tgttatc	atg	ctg	aag	ctt	tta	ggc	gtg	ctt	att	ttg									578
		Met	Leu	Lys	Leu	Leu	Gly	Ala	Val	Leu	Ile	Leu								
		1				5				10										
gca	gca	gcc	aca	tgg	aca	gga	ttt	gaa	atg	gcg	aag	cct	ttc	agg	gaa					626
Ala	Ala	Ala	Thr	Trp	Thr	Gly	Phe	Glu	Met	Ala	Lys	Pro	Phe	Arg	Glu					
			15					20					25							
agg	ccg	aag	caa	atc	cgc	cag	ctg	ttg	gcc	gct	ttg	cag	tct	ttg	gag					674
Arg	Pro	Lys	Gln	Ile	Arg	Gln	Leu	Leu	Ala	Ala	Leu	Gln	Ser	Leu	Glu					
		30					35					40								
gct	gaa	atc	atg	tac	ggg	cat	aca	ccg	ctc	cgt	cag	gca	tca	aaa	cag					722
Ala	Glu	Ile	Met	Tyr	Gly	His	Thr	Pro	Leu	Arg	Gln	Ala	Ser	Lys	Gln					
	45					50					55									
atc	gca	cac	cag	ctt	acc	gag	ccg	gta	gcc	tct	ttg	ttt	cag	aca	ttt					770
Ile	Ala	His	Gln	Leu	Thr	Glu	Pro	Val	Ala	Ser	Leu	Phe	Gln	Thr	Phe					
					65					70					75					
60.																				
gca	gaa	cag	ctt	gaa	aaa	ggc	agc	gct	tca	gca	ggg	acg	gca	tgg	gaa					818
Ala	Glu	Gln	Leu	Glu	Lys	Gly	Ser	Ala	Ser	Ala	Gly	Thr	Ala	Trp	Glu					
				80					85					90						
gac	agc	ctg	gag	aaa	gta	tgg	ccc	gaa	acg	gct	ctt	aaa	aag	aaa	gaa					866
Asp	Ser	Leu	Glu	Lys	Val	Trp	Pro	Glu	Thr	Ala	Leu	Lys	Lys	Lys	Glu					
			95					100					105							
tac	gag	att	tta	cgg	caa	ttc	ggc	gaa	acg	ctg	ggc	cgt	cat	gat	ctg					914
Tyr	Glu	Ile	Leu	Arg	Gln	Phe	Gly	Glu	Thr	Leu	Gly	Arg	His	Asp	Leu					
		110					115					120								
att	tct	cag	caa	aaa	cat	atc	aaa	ctg	gcg	tta	acc	cat	tta	gag	aca					962
Ile	Ser	Gln	Gln	Lys	His	Ile	Lys	Leu	Ala											

10295.204.ST25.txt

ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc 1206
 Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe
 215 220 225
 caa aag ata aaa gct gtc ttt cta ttt caa gga taggggggct cactc att 1257
 Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly Ile
 230 235 240
 gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc 1305
 Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser
 245 250 255
 ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt 1353
 Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val
 260 265 270
 ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa 1401
 Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu
 275 280 285
 atc att cgg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg 1449
 Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met
 290 295 300
 atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg 1497
 Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala
 305 310 315 320
 gag ttt ggc gcc ca 1511
 Glu Phe Gly Ala

<210> 55
 <211> 171
 <212> PRT
 <213> Bacillus licheniformis

<400> 55

Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu Ala Ala Ala Thr Trp
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Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile
20 25 30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr
35 40 45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu
50 55 60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu
65 70 75 80

Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys
85 90 95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg
100 105 110

10295.204.ST25.txt

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys
 115 120 125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala
 130 135 140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe
 145 150 155 160

Leu Thr Gly Leu Leu Ile Leu Leu Leu Met
 165 170

<210> 56
 <211> 68
 <212> PRT
 <213> Bacillus licheniformis

<400> 56

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 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
 50 55 60

Leu Phe Gln Gly
 65

<210> 57
 <211> 85
 <212> PRT
 <213> Bacillus licheniformis

<400> 57

Ile Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu
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Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val
 20 25 30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr
 35 40 45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn
 50 55 60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile
 65 70 75 80

10295.204.ST25.txt

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<210> 58
<211> 1207
<212> DNA
<213> Bacillus licheniformis
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10295.204.ST25.txt

1207

ttc

<210> 59
 <211> 68
 <212> PRT
 <213> Bacillus licheniformis

<400> 59

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Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
 50 55 60

Leu Phe Gln Gly
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 <212> DNA
 <213> Bacillus licheniformis

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 tttttgccgg ctgcacgatt tttttattct tagtagatca ggtctacgaa atcattcgga 240
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 agattatcgg gattgcttat attgcggagt ttggcgccca gctgacaaag gatgccggac 360
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 tgcctatttt aaccgtgatt atcgaaacga tcatcggaact catcccttcc atgtcttagt 480
 cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc 533
 Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile
 1 5 10
 gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa 581
 Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu
 15 20 25
 gcg gag ccg gct ggg gaa acc gct gca gaa gaa tcg gca gaa gcc att 629
 Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Ser Ala Glu Ala Ile

10295.204.ST25.txt

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tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln 60 65 70 75			725
aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro 80 85 90			773
gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu 95 100 105			821
gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys 110 115 120			869
gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser 125 130 135			917
aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu 140 145 150 155			965
aac agc ttt cgg gtt gcc gtc aca tat gcg aat gaa gcg att cag acg Asn Ser Phe Arg Val Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr 160 165 170			1013
atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met 175 180 185			1061
gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile 190 195 200			1109
ctt ttt ctc atg aac acg agc ggc ttg ttt atc caa tat atc gtg ttg Leu Phe Leu Met Asn Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu 205 210 215			1157
ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr 220 225 230 235			1205
gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala 240 245 250			1253
atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser 255 260 265			1301
gtt cag ggc gcc tca gcc gca gtg acg gac ggc att act ttg cgg acg Val Gln Gly Ala Ser Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr 270 275 280			1349
gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe 285 290 295			1397
acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn 300 305 310 315 320 325 330 335 340 345 350			1445

10295.204.ST25.txt
310

300 305 315
 acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt 1493
 Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe 330
 320
 ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg 1541
 Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala 345
 335
 gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat 1589
 Ala Val Leu Gln Pro Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp 360
 350
 gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt 1637
 Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val 375
 365
 tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat 1685
 Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn 390
 380 385 395
 ctg acg atg atg atg aag tagggagggg tgagatggaa tttctgacag 1733
 Leu Thr Met Met Met Lys 400
 agtggctcac gaatattatt ctatttattc tgatggcgat cgtcatcgat atgcttctgc 1793
 cgaattcgag catgcaaaaa tacgcgaaaa tggatgatcag cctgctcttg atcggtgttaa 1853
 tactgaaccc gatcttctct ttattcagga cagatccgga tgtgattttt gagaagctta 1913
 caaaaaacgg acaagttcag tcaaacgaaa taaaaaatca gctgaattca gaaaaaaaag 1973
 aaatacaagc ctcaacaaca gcatatatct tagaacagat ggctgttcaa ttggaaaaga 2033
 acgcagaggg caggtttaca agcgacaaat acaagataga ccgagtcgag gtctcttctg 2093
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 <211> 401
 <212> PRT
 <213> Bacillus licheniformis
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 20 25
 Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala 45
 35 40
 Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu 60
 50 55
 Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu 80
 65 70 75

10295.204.ST25.txt

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys
85 90 95

Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu
100 105 110

Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu
115 120 125

Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala
130 135 140

Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val
145 150 155 160

Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile
165 170 175

Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly
180 185 190

Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn
195 200 205

Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu
210 215 220

Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val
225 230 235 240

Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala
245 250 255

Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser
260 265 270

Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr
275 280 285

Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp
290 295 300

Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu
305 310 315 320

Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile
325 330 335

Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Ala Val Leu Gln Pro
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Tyr His Tyr 30 Phe Leu Leu Leu 35 Phe Val Leu Gly Val 40 Ser Phe Met Leu 629

gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat 677
Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp
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gag ccg gcg gct tca caa aaa gct acg tct gaa agc acc gta cag agc 725
 Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser 75

ggt gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg 773
Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro
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 Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val
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 Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr
 125 130 135

cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg 965
 Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr
 140 145 150 155

gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga 1013
 Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly
 160 165 170

gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg 1061
 Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg
 175 180 185

ggt gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag 1109
 Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys
 190 195 200

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 Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg
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 Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser
 220 225 230

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<400> 63

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Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys
 65 70 75 80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln
 85 90 95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr
 100 105 110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr
 115 120 125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr
 130 135 140

Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr Val Ser Glu Met Ser
 145 150 155 160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro
 165 170 175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val
 180 185 190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala
 195 200 205

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 210 215 220

Lys Lys Met Lys Glu Asp Ser
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Page 88

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Val Val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys
35 40 45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro
50 55 60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser
65 70 75 80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp
85 90 95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser
100 105 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr
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aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaa 180
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gttctcagca cgaacccgat ggatttttta aaacaagaaa cggcccctgg gcagacgctt 360
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Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys
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caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga 581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly
15 20 25

tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta 629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val
30 35 40

gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg 677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp
45 50 55

ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt 725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe
60 65 70 75

tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt 773
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu
80 85 90

tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt 821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Ser His Val Gln Leu Phe
95 100 105

cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa 869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln
110 115 120

aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg 917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser
125 130 135

cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca 965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser
140 145 150 155

tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg 1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu
160 165 170

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Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr
175 180 185

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190 195 200

cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa 1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys
205 210 215

aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct 1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser
220 225 230 235

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa 1253
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240 245 250

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Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu
255 260 265

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aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490	1973
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gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile 590 595 600	2309
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cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu 640 645 650	2453
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro 655 660 665	2501
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tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg ccg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745	2741
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35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
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180 185 190

10295.204.ST25.txt

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
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 245 250 255
 Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
 260 265 270
 Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
 275 280 285
 Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
 290 295 300
 Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
 305 310 315 320
 His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
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 Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
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 405 410 415
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10295.204.ST25.txt

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500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
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545 550 555 560

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610 615 620

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Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

WO 03/087148

10295.204.ST25.txt

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 <213> Bacillus licheniformis

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 caa cat atg aag gac cat ctg tcg atc tat tta ttt gtt tct gtg ctg 581
 Gln His Met Lys Asp His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu 25
 15
 ttc tta atg ggt gtg att ttc ggc gcg gtc atc gtc aac agc atg acg 629
 Phe Leu Met Gly Val Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr 40
 30
 atc ggt caa aaa gaa gat ttg ttc tac tat ttg aat caa ttt ttt gga 677
 Ile Gly Gln Lys Glu Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly 55
 45
 cag ctt tcc gaa gga aaa gca gcc agc tca aag gaa atg ttt ttg cag 725
 Gln Leu Ser Glu Gly Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln 75
 60
 agc ttt ctt cat aat atg aaa tat tta ggc tta atg tgg att ctc ggg 773
 Ser Phe Leu His Asn Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly 90
 80
 ata tcc atc atc ggt ctg ccc gtc att ttt atc atg gtc ttc tta aaa 821
 Ile Ser Ile Ile Gly Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys 105
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10295.204.ST25.txt

ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga	869
Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly	
110 115 120	
atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att	917
Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile	
125 130 135	
ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt	965
Leu Leu Ile Pro Ala Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe	
140 145 150 155	
tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc	1013
Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser	
160 165 170	
acc tgt cca tgt gtt gtg ccg cgg gta gcc ga	1045
Thr Cys Pro Cys Val Val Pro Arg Val Ala	
175 180	

<210> 69
 <211> 181
 <212> PRT
 <213> Bacillus licheniformis

<400> 69

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 1 5 10 15

His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val
 20 25 30

Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu
 35 40 45

Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly
 50 55 60

Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn
 65 70 75 80

Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly
 85 90 95

Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly
 100 105 110

Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe
 115 120 125

Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala
 130 135 140

Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile
 145 150 155 160

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10295.204.ST25.txt
 Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val
 165 170 175

Val Pro Arg Val Ala
 180

<210> 70
 <211> 1108
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (500)..(1108)

<400> 70
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 aagagagatg agagacgaca gtccgtccag gtcgctcggt cccgcgggga tgagctttgg 120
 gaaaagaaag gtcctcaccg aagaagacct tcccgatgaa gagcaccgca aatcgtttct 180
 cggatatagtc ggaggcctcg cagaggatga aaaaaggcag ctgatccatg aagtcctcgc 240
 tccgctcggc cataacttaa tggtgacccc taaagaggtc gatacattta tcgatgatat 300
 ggcaaagtgt attgcaaacg gtctgaacac agcgctccat gaaaatgtat cgcaagacaa 360
 taaaggaatg tataaccact aagatcaagg cggctggccc ggccgctttt tttcatgaca 420
 tttagcattg ccggaacttg ttctacttcc tctatcttgt acatagtcta tttactagac 480
 aagctctgga gggatttac aat gag aaa aag agg cag gaa tcg tca gtt tgt 532
 Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys 10
 1
 gct ggc tgt aaa tgg aag aag cgc ggt tca gac agt att ctt att tat 580
 Ala Gly Cys Lys Trp Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr 25
 15
 cgt cag cct gct gct cgt ttt tat ttt atc agg cgt gct cac atc gct 628
 Arg Gln Pro Ala Ala Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala 40
 30
 gcg tcc tca gtt aag gcc gtc ttc atc gtt gta ccg ggt ggc tca tca 676
 Ala Ser Ser Val Lys Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser 55
 45
 act gaa ggg cga gac ctt tgg gct cat ttt ggg aat gga aaa cca cta 724
 Thr Glu Gly Arg Asp Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu 75
 60
 ctt tgc atc aga att gcc gga acc gaa tca gcg ctt tca gct ttc ccc 772
 Leu Cys Ile Arg Ile Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro 90
 80
 cct cgt cct gaa gct gcc gac cag cat tca ttt gaa aga tcc gcg aag 820
 Pro Arg Pro Glu Ala Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys 105
 95
 ttt tct cgg acg gga gct tcc ggg att ctc tca ttt tca ctc gga aat 868
 Phe Ser Arg Thr Gly Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn 120
 110
 cct cat tgc cgg gca agg gac gga tta tac gaa tat gcc gtc aga atc 916
 Page 98

10295.204.ST25.txt

Pro His Cys Arg Ala Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile
 125 130 135

tcc gcc gcc gac tca ggt ctt aaa aga gga gag aga agc gaa tct tgc 964
 Ser Ala Ala Asp Ser Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys
 140 145 150 155

aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc 1012
 Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser
 160 165 170

tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca 1060
 Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala
 175 180 185

caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt 1108
 Gln Tyr Gly Ile Val Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
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<210> 71

<211> 203

<212> PRT

<213> Bacillus licheniformis

<400> 71

Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys Ala Gly Cys Lys Trp
 1 5 10 15

Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr Arg Gln Pro Ala Ala
 20 25 30

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys
 35 40 45

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp
 50 55 60

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile
 65 70 75 80

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala
 85 90 95

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly
 100 105 110

Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala
 115 120 125

Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser
 130 135 140

Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu
 145 150 155 160

Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly
 Page 99

10295.204.ST25.txt
170

175

165

Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val
180 185 190

Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
195 200

<210> 72
<211> 1152
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (107)..(985)

<400> 72
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taaaagtata aatttcacatga agagggttca gaatgggtgct gaggtg atg agt aag 115
Met Ser Lys
1

aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa 163
Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln
5 10 15

ttt ttt cgt aaa cgc tgg gta ttt ccg gcc atc tat ttg aca agt gcc 211
Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala
20 25 30 35

gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac 259
Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn
40 45 50

gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat 307
Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp
55 60 65

aac cgg gat gat gcg gta gaa gta ggc aaa cca gtc gaa aat gtc gca 355
Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala
70 75 80

atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt 403
Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe
85 90 95

gaa act gac gca act aaa gaa gag aaa gaa gca gca ctt gta aac tat 451
Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu Val Asn Tyr
100 105 110 115

aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac 499
Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp
120 125 130

gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa 547
Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys
135 140 145

gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa 595
Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu
150 155 160

10295.204.ST25.txt

gat ggt tta tca act gtg tat cag tct ctt tct gaa gta agc gtc aaa 643
 Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys
 165 170 175
 caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa 691
 Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys
 180 185 190 195
 aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc 739
 Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe Glu Ile Arg
 200 205 210
 aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc 787
 Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val
 215 220 225
 tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa 835
 Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu
 230 235 240
 cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg 883
 Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala
 245 250 255
 aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg 931
 Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser
 260 265 270 275
 tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc 979
 Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser
 280 285 290
 cag tca taaggcacgc ttccctcagg gcgcctatca aatgcgatag gcgccttttt 1035
 Gln Ser
 tgttacaatc aaaaaaaacc cgtatcaaat cggcggagcc agccgttttt aagtaagagg 1095
 cctctttaag gagtggaagg cattaggaag taagtagaac agcaaaccgc ctagtaa 1152

<210> 73
 <211> 293
 <212> PRT
 <213> *Bacillus licheniformis*.

<400> 73

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1 5 10 15

Leu Gln Gln Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu
20 25 30

Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala
35 40 45

Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser
50 55 60

Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu
65 70 75 80

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10295.204.ST25.txt

Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys
 85 90 95
 Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu
 100 105 110
 Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala
 115 120 125
 Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr
 130 135 140
 Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val
 145 150 155 160
 Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val
 165 170 175
 Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys
 180 185 190
 Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe
 195 200 205
 Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp
 210 215 220
 Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu
 225 230 235 240
 Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu
 245 250 255
 Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg
 260 265 270
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 275 280 285
 Asp Ser Ser Gln Ser
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<210> 74
 <211> 1747
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1244)

<400> 74
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10295.204.ST25.txt

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ctcatcatct ttggcgcgac gatcgtccat ttgcctgtca gcacgacaca cgtcatttct 240
tcattccattt taggcgtggg cgcttcccac cgggtgaaag gcgtaaactg gggcaccgca 300
aagcggatgc tgatcacttg ggtcattacc cttcccatct cggcaaccat cgggtgcattt 360
gcctattttca tacttgattt attcttttaa tcagcacact cccgtccgaa tctaggacgg 420
gagttttcat gtttaaaaga aagccggcat aacaatagaa ataggaactg cactatttct 480
cgggaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt 533
                Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu
                1                    5                    10

att gtt ttg gcg ctg gct ctg tac gta gct gcc gtg tgg cgt ttt gaa 581
Ile Val Leu Ala Leu Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu
                15                    20                    25

aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt 629
Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu
                30                    35                    40

ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca 677
Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser
                45                    50                    55

att ttc aca aac ccg ctt cat tac ctg atc gtt gcc gtt ttt ttc acg 725
Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr
        60                    65                    70                    75

ttg aca gac gct ttt att ttc tta aat gcc tac ttt aaa aag ctc ggc 773
Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly
                80                    85                    90

agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac 821
Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn
                95                    100                    105

gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta 869
Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu
                110                    115                    120

ttg aaa aac gaa ccg atc cac atc tat tat gga aat ata gaa gcg tat 917
Leu Lys Asn Glu Pro Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr
                125                    130                    135

gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat 965
Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn
        140                    145                    150                    155

ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat 1013
Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His
                160                    165                    170

ttg ctt gag cat atg gaa aac cgg ttc gat gtt caa gaa aag ctt gac 1061
Leu Leu Glu His Met Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp
                175                    180                    185

cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct 1109
Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro
                190                    195                    200

ttt tcc atc cac gat ttt gac tat gtc atg aag tta acc tca gaa gac 1157

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10295.204.ST25.txt

Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp
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 Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile
 220 225 230 235

tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc
 Tyr Asp Leu Leu 240 Leu Pro Asn Glu Glu Glu Gly Asp Asp 245 1254

tgcttttcag caagaccagg aaagcgtaaa aaagcgcttc gccttttaaaa tgttttaaag 1314

gcaatccaaa accaatatcg cgaaatacga agtcagcccc tataccgaac ggattttccg 1374

gcaaaacgaa cggctgatcg gcgagtataa aagaaaaaaa gcttaacgag gacgggaaaa 1434

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gcaaaattcg gcctgtcaga ctatacctct ctcttcagaa gaagaagcga aaaaatcatt 1614

aaaacgctga acagaagaaa aaacaaaccg tgaagcttgg actttcaccc tccttctctg 1674

ctgagaaggg gggttatttt catgtctaca ggagcatcat aaaggatgcc cctgtccgcc 1734

ttctcctaca gat 1747

<210> 75
 <211> 248
 <212> PRT
 <213> Bacillus licheniformis

<400> 75

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Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly
 35 40 45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro
 50 55 60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe
 65 70 75 80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala
 85 90 95

Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr
 100 105 110

Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro
 115 120 125

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10295.204.ST25.txt

caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att	629
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30 35 40	
gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt	677
Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly	
45 50 55	
cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt	725
Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe	
60 65 70 75	
caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta	773
Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu	
80 85 90	
gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc	821
Asp Thr Leu Thr Leu Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe	
95 100 105	
atc tct tac tct gaa aac ttt gat aca ggc agt cca att ggt cgt tta	869
Ile Ser Tyr Ser Glu Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu	
110 115 120	
gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta	917
Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu	
125 130 135	
tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca	965
Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser	
140 145 150 155	
tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt	1013
Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu	
160 165 170	
gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta	1061
Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu	
175 180 185	
tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa	1109
Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys	
190 195 200	
gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta	1157
Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val	
205 210 215	
gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta	1205
Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu	
220 225 230 235	
aaa gtt gaa aat tgg gat aca aaa cgg agg aga ggg aaa aat cca aat	1253
Lys Val Glu Asn Trp Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn	
240 245 250	
cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta	1301
Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu	
255 260 265	
tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg	1349
Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg	
270 275 280	
caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat	1397
Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp	
285 290 295	

10295.204.ST25.txt

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 300 305 310 315

gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac 1493
 Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn
 320 325 330

aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca 1541
 Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala
 335 340 345

gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat 1589
 Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn
 350 355 360

cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct 1637
 Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser
 365 370 375

tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca 1685
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 380 385 390 395

gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga 1733
 Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg
 400 405 410

cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga 1782
 Pro Tyr Gln

aaaagcagag ttagaacaaa ggcacaatga atcactgggc aattaagctc gaacgatgca 1842
 aaagtaataa aaccagaact gattcaaaaag ctttagaaaa aattccttta gtctataaac 1902
 atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca 1962
 atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcattatt 2020

<210> 77
 <211> 414
 <212> PRT
 <213> Bacillus licheniformis

<400> 77

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 1 5 10 15

Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala Gln Leu Gln Thr Leu
 20 25 30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val
 35 40 45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln
 50 55 60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val
 65 70 75 80

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10295.204.ST25.txt

Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Thr Leu
 85 90 95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu
 100 105 110

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met
 115 120 125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys
 130 135 140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val
 145 150 155 160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys
 165 170 175

Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys
 180 185 190

Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr
 195 200 205

Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp
 210 215 220

Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp
 225 230 235 240

Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu
 245 250 255

Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln
 260 265 270

Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro
 275 280 285

Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met
 290 295 300

Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys
 305 310 315 320

Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala
 325 330 335

Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile
 340 345 350

10295.204.ST25.txt

Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn Gln Leu Phe Ser Lys
 355 360 365

Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser Leu Asn Gln Leu Asn
 370 375 380

Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser Glu Ile Gln Glu Tyr
 385 390 395 400

Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg Pro Tyr Gln
 405 410

<210> 78
 <211> 1417
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (510)..(1298)

<400> 78
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 ctgaatgaat cagggtaaat tcggtttttt ctgcagaaag ctctttcaat tcaaattgtga 120
 cgatccatcc cgacgtatcc cagctgaaag cgagtcgatg cggcgcacatca agctcgatca 180
 ctttgacagg ggagggggccg aaaggagact gcagggtgaa ttcgcagccg atctccgggc 240
 ggaaatcatt aggcataaac caggcggcga tgccttcact ggtggcgacg gcctcccaca 300
 ctttttctat cgatgcgtga aaaacagcct gtttatgtat atcaggcact agttgattgc 360
 tcataataga cctcctagaa aaaagtaaaa ccaaatgggtt tcctttctat tatatgaaac 420
 ctttttagttt tatgtcaatg ttccgtcata attccctggg acaaggcata tcattgaaca 480
 aacgaacctg aatgtaaagg atgagggtt atg agt cat aga gca gat gag att 533
 Met Ser His Arg Ala Asp Glu Ile
 1 5
 cga aaa aga atg gcc agg aaa aga aag cgg aaa aca ccg gac aaa cag 581
 Arg Lys Arg Met Ala Arg Lys Arg Lys Arg Lys Thr Pro Asp Lys Gln
 10 15 20
 ccc ttt tca tca gac ggc aaa aag cgg ccg ctc aag ccg cct gca tgg 629
 Pro Phe Ser Ser Asp Gly Lys Lys Arg Pro Leu Lys Pro Pro Ala Trp
 25 30 35 40
 aca gcc ttt tcg gaa gat gaa aaa gga gga gac ttc cct ccg cct gaa 677
 Thr Ala Phe Ser Glu Asp Glu Lys Gly Gly Asp Phe Pro Pro Pro Glu
 45 50 55
 gga agt tcc ctg ctg ata aac ggg aag cac ccg ctt gtc aag gcg gat 725
 Gly Ser Ser Leu Leu Ile Asn Gly Lys His Pro Leu Val Lys Ala Asp
 60 65 70
 gcg ctc atc ttg aaa tgt ctt ctg tcg gca tgc ctt gtt ctt gtg tcc 773
 Ala Leu Ile Leu Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser
 75 80 85
 gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg 821
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Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro
 90 95 100 869

gtt atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag
 Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln
 105 110 115 120

aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg
 Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro
 125 130 135 917

aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct
 Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala
 140 145 150 965

gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag ggc att
 Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile
 155 160 165 1013

aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat
 Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr
 170 175 180 1061

gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg
 Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu
 185 190 195 200 1109

cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg
 Gln His Ala Asp Asn Ser Tyr Thr Tyr Tyr Gly Gln Leu Lys Lys Ala
 205 210 215 1157

gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg
 Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr
 220 225 230 1205

att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa
 Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys
 235 240 245 1253

caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag
 Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu
 250 255 260 1298

taaattggacg gagctcttca ccaagcttca cattcatccg ctgctgtggc ttgtcatggc
 1358

gacggtatc atgacaggac atattaaagg cgcgtgtttt gtttaatgca cccaggaag
 1417

<210> 79
 <211> 263
 <212> PRT
 <213> Bacillus licheniformis

<400> 79

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 1 5 10 15

Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys
 20 25 30

Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys
 35 40 45

Gly Gly Asp Phe Pro Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly
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10295.204.ST25.txt
60

50

55

Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu
65 70 75 80

Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe
85 90 95

Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu
100 105 110

Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly
115 120 125

Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln
130 135 140

Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln
145 150 155 160

Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr
165 170 175

Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro
180 185 190

Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr
195 200 205

Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile
210 215 220

Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys
225 230 235 240

Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro
245 250 255

Ile Gln Val Ile Thr Phe Glu
260

<210> 80
<211> 1468
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (982)..(1428)

<400> 80
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10295.204.ST25.txt

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tgaagctgta cataaatcgt ttcctgacct tgatgtccaa accgtcggcg gttctgaaac 180
catcgtggag atccaatatc cgaaaagggg tctgtcggcc gtgcttttca tcgccgtctg 240
gctgctcttg ttcgtcgggtg ccggccttgc cgtcatgaac tttcatgaag atgtcagcat 300
gaggggaagtg cacatcctgc tttacgaaat ggtgacgggc aagggtgaacc gctatccata 360
ccttttgcag gttccgtaca gcatcgggtct tggcctcggc atgatcttgt tttttaataca 420
tttatttaaa aaacggttta acgaggagcc cagccccctg gaggtcgaga tgtttaataa 480
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tcatgatcat tagcgtgata tttatcatct ttctcggact cgcaggaggg gttgctgttg 600
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cgaaaacaaa aggatttatc caggcgtatg aatgggctgt ctttttaggc gcggttttcg 720
gaggatggga atcgtgaac atgtcccgt ttttttatc caaatggctg cttgttccga 780
tcggcctttt tgcgggcgtt ttcattggaa tgcttcagc ggcgctaaca gaagtcttga 840
acgtgctgcc gatactggcg aaacgcatcg ggatgggaga ccggattttg ataattttaa 900
tggccattgt tttcggcaag attctcggat cgatgttcca atggctcatt tttgttcatt 960
tgtcataaaa ggaggattat g atg tca agt ttg aaa gat aat tat caa tcg 1011
Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser 10
1
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc 1059
Lys Val Lys Ala Tyr Gln Pro Ser Pro Tyr Val Leu Asn Cys Ile 25
15
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc 1107
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe 40
30
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg 1155
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly 55
45
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc 1203
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly 70
60
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc 1251
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala 90
75
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag 1299
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu 105
95
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag 1347
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys 120
110
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg 1395
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val 135
125
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa 1448
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe

10295.204.ST25.txt

140

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attaacagga aaacaaacat

1468

<210> 81
 <211> 149
 <212> PRT
 <213> Bacillus licheniformis

<400> 81

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
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 20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
 130 135 140

Phe Asp Lys Leu Phe
 145

<210> 82
 <211> 1453
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (504)..(950)

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tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccagggc tgactcagct 180

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gacgaaaaca aaaggattta tccaggcgta tgaatgggct gtcatttttag gcgcggtttt	240
cggaggatgg gaatcgctga acatgtcccg ctttttttta tccaaatggc tgcttggtcc	300
gatcggcctt tttgcgggcg ttttcattgg aatgcttgca gcggcgctaa cagaagtctt	360
gaacgtgctg ccgatactgg cgaaacgcat cgggatggga gaccggattt tgatactttt	420
aatggccatt gttttcggca agattctcgg atcgatgttc caatggctca tttttgttca	480
tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser 1 5 10	533
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile 15 20 25	581
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe 30 35 40	629
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly 45 50 55	677
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly 60 65 70	725
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala 75 80 85 90	773
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu 95 100 105	821
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys 110 115 120	869
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val 125 130 135	917
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe 140 145	970
attaacagga aaacaaacat gggaattcga gaacccgctg tttgttaact caagcggaac	1030
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gttgattgac ggggggtttcg caaagcgcgc cctagcggca accagcagcc ataatgctac	1390
ggcagaaaagg cagttccgct acccgacgga atacgggggg caaaaaccgg gaaccgcgac	1450
ttc	1453

10295.204.ST25.txt

<210> 83
 <211> 149
 <212> PRT
 <213> Bacillus licheniformis

<400> 83

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 20 25 30

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 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
 130 135 140

Phe Asp Lys Leu Phe
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<210> 84
 <211> 2020
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1517)

<400> 84
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 catttctcgt cgggtgtctg atttgtacga tcggccaggc tttccagaat ttttatatgg 180
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10295.204.ST25.txt

tctccgctct gttaacaggc cttggcgtct acgacagaat cggacagttt gccggcgctg 300
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 aaagcgaaag ctacgtcctc ggcgtatgga caaacatggt caagcttgcg ggaaacgtca 420
 tcgtgttcgg tggtgtggcc gcttatattg tggggatgat ccgctttgcc tttgacaagc 480
 tgttttagga ggaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc 533
 Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe
 1 5 10
 gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa 581
 Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys
 15 20 25
 gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa 629
 Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu
 30 35 40
 atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg 677
 Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met
 45 50 55
 gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa 725
 Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu
 60 65 70 75
 gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca 773
 Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr
 80 85 90
 gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt 821
 Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe
 95 100 105
 gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg 869
 Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu
 110 115 120
 att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat 917
 Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His
 125 130 135
 aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg 965
 Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly
 140 145 150 155
 caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc 1013
 Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val
 160 165 170
 gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc 1061
 Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val
 175 180 185
 gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg 1109
 Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser
 190 195 200
 gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat 1157
 Ala Met Ala Pro Ala Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp
 205 210 215
 ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt 1205
 Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu
 220 225 230 235

10295.204.ST25.txt

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cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala 270 275 280	1349
gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu 285 290 295	1397
aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc Asn Arg Val Leu Val Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile 300 305 310 315	1445
atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe 320 325 330	1493
gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcattg cttttattgc Glu Arg Ala Glu Arg Gly Asn Ala 335	1547
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gatatttgaa ctgacatctg ccggtatatc tgccgctatc ttgttcgctt ttcttgttgc	1847
cgtgattttt aaaccgaaag gataaaggaa aatgccagca aaacgcaagg tcattttggt	1907
cacagacggc gatataacg ctgcaaaagc aatcgaatat gcagcaagaa aaacgggtgg	1967
ccgctgcatt tcccaatcgg cggggaatcc gagcgttaaa acaggaccgg agc	2020

<210> 85
 <211> 339
 <212> PRT
 <213> Bacillus licheniformis

<400> 85

Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe Glu Asn Pro Leu Phe 1 5 10 15
Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro 20 25 30
Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln 35 40 45
Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln 50 55 60

10295.204.ST25.txt

Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe
65 70 75 80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala
85 90 95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr
100 105 110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe
115 120 125

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu
130 135 140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr
145 150 155 160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln
165 170 175

Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp
180 185 190

Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala
195 200 205

Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro
210 215 220

Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser
225 230 235 240

Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr
245 250 255

Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val
260 265 270

Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala
275 280 285

His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val
290 295 300

Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu
305 310 315 320

Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg
325 330 335

Gly Asn Ala

<400>	86															60
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cgtaaa	aca	ggacc	ggagc	ttgta	accat	gac	cctgcaa	acccct	catg	atc	ctgtatt					180
cg	catgttt	gatgat	tccg	gactt	caagg	tgaag	ggccg	ggagag	acag	ctatg	aaata					240
tgtag	cgatg	catccc	gata	tcgag	gtgct	cggag	tc	atc	gccgt	cgtt	caaaa	actca				300
ttatg	cagag	tggac	gagag	tcgat	gtatc	aatc	gatgca	gaagg	cgaac	tgac	agagta					360
cg	cg	tcgat	aaacac	gggg	tcaa	agagtt	cgatgt	caaa	cgaat	gaatg	gtgata	acagt				420
ctatt	gcctt	gaccag	ctgg	atgtt	ccgat	cattg	tcgga	atc	gg	tgata	tcg	gtaagat				480
gaacag	aaaa	gacgat	gtgg	aaaa	aggttc	gccg	attaca	atgaa	agcgg	tcgag	ctcat					533
tttag	aaagg	agcgg	gtatc	atg	agt	gct	caa	aag	caa	gag	aag	acg	aac	gta		
				Met	Ser	Ala	Gln	Lys	Gln	Glu	Lys	Thr	Asn	Val		
				1				5					10			
ttc	ctt	gat	cct	tct	aag	aat	gaa	gcg	tat	ttc	aag	aag	cgg	gtc	ggc	581
Phe	Leu	Asp	Pro	Ser	Lys	Asn	Glu	Ala	Tyr	Phe	Lys	Lys	Arg	Val	Gly	
			15					20					25			
atg	gga	gaa	agc	ttt	gac	ctt	ggc	gta	cgg	aag	gtc	ttt	att	ctc	gga	629
Met	Gly	Glu	Ser	Phe	Asp	Leu	Gly	Val	Arg	Lys	Val	Phe	Ile	Leu	Gly	
		30					35					40				
cat	gaa	gtt	cag	ctt	tat	tat	gtc	aac	gga	ttg	tgc	gac	aca	caa	tac	677
His	Glu	Val	Gln	Leu	Tyr	Tyr	Val	Asn	Gly	Leu	Cys	Asp	Thr	Gln	Tyr	
	45					50					55					
atc	att	cac	ctg	tta	aga	gaa	ctg	gtg	cat	ctg	aat	gat	aaa	gaa	aaa	725
Ile	Ile	His	Leu	Leu	Arg	Glu	Leu	Val	His	Leu	Asn	Asp	Lys	Glu	Lys	
					65					70					75	
gaa	tcg	ggc	gag	gtc	gaa	gac	atc	gtc	gaa	aac	agg	ctt	ttg	aac	cag	773
Glu	Ser	Gly	Glu	Val	Glu	Asp	Ile	Val	Glu	Asn	Arg	Leu	Leu	Asn	Gln	
				80					85					90		
cag	gtt	tca	aaa	gcg	gaa	acg	ctt	gat	gaa	gct	gtc	gac	caa	gtg	ttg	821
Gln	Val	Ser	Lys	Ala	Glu	Thr	Leu	Asp	Glu	Ala	Val	Asp	Gln	Val	Leu	
			95					100					105			
tca	gga	ctg	gtt	gcc	atc	atc	gtc	gaa	gat	gcg	ggc	ttt	gct	ttt	atc	869
Ser	Gly	Leu	Val	Ala	Ile	Ile	Val	Glu	Asp	Ala	Gly	Phe	Ala	Phe	Ile	
		110					115					120				
atc	gat	gtc	aga	agc	tac	ccg	ggc	aga	acg	ccg	gaa	gaa	cct	gat</		

10295.204.ST25.txt

Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile
 140 145 150 155
 1013
 gtc aac aca gcc ctg att aga cgc cgg atc aga gat gag cgc ttg cgc
 Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg
 160 165 170
 1061
 tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc
 Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu
 175 180 185
 1109
 tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa
 Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys
 190 195 200
 1157
 aaa gaa att gaa gat gtg aag atc gac ggg ctg ccg atg tcg gat aaa
 Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys
 205 210 215
 1205
 tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt
 Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu
 220 225 230 235
 1253
 gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag
 Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu
 240 245 250
 1301
 ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca
 Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr
 255 260 265
 1349
 ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag
 Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Glu Tyr Arg Gln
 270 275 280
 1397
 acg ccg gct gtt ggg acg ttt tta agg tgg gtg ccg ttt ttc ggt att
 Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile
 285 290 295
 1445
 ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat
 Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His
 300 305 310 315
 1493
 ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac
 Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp
 320 325 330
 1541
 acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc
 Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val
 335 340 345
 1589
 gaa ttt tta aga atg gcc gcc att cat acg ccg acg gcg ctt tcg act
 Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr
 350 355 360
 1637
 gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc gcg atc aat
 Ala Met Gly Leu Ile Ala Val Leu Ile Gly Asp Ile Ala Ile Asn
 365 370 375
 1685
 gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca
 Val Gly Leu Phe Ser Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala
 380 385 390 395
 1733
 atc gga gcc tac acg aca cca agc tac gag ctg agc ctg gcg aat aaa
 Ile Gly Ala Tyr Thr Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys
 400 405 410
 1781
 atg gtg aag ctg ttt atg ctg ata ttg gtc gcg ctt ttt aaa gtg gag

10295.204.ST25.txt

Met Val Lys Leu Phe Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu
 415 420 425

gga ttt gtc atc gga tta acg atc tta act ata gtg atg act tcg atc 1829
 Gly Phe Val Ile Gly Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile
 430 435 440

agg tca ttg cga acg cct tac tta tgg cct ctc ctc ccg ttc aat gga 1877
 Arg Ser Leu Arg Thr Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly
 445 450 455

aaa gcg ttt tgg cat gtt ctc gtg cgc acg tcc gtt cca ggg gga aaa 1925
 Lys Ala Phe Trp His Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys
 460 465 470 475

gtc agg ccg agc atc gtt cat ccg aga aac cgc tcc aga cag ccg 1970
 Val Arg Pro Ser Ile Val His Pro Arg Asn Arg Ser Arg Gln Pro
 480 485 490

tgaagccggc attcgaagag gcttttcccc ggggaaaagc ctctttttca ataatcgaat 2030
 tccgggtcttt gaggaccgat gcctctgtat tcattggcag agatcgcgac tgcccggagg 2090
 ctgcagatgt tggtctgtct tctgatcgga tagacgacat acagcatttc gcggccgtac 2150
 ggggtcaatcg ttgacgaatg aaggaaaacc tcagttcctc tccgccaaaa tctcgtattc 2210
 gccggagctg taataatctg cccctcataa ggctcataaa ttctctgttc ataatgcgca 2270
 gccggctgat aaggggcgta tacatcttca ggtgcatagc cgggagcggg ggtgtaggga 2330
 taacgatttg gatacatatg ataacctctt tcccacttcg ttttttggtt ttcattctta 2390
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<210> 87
 <211> 490
 <212> PRT
 <213> Bacillus licheniformis

<400> 87

Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val Phe Leu Asp Pro Ser
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Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly Met Gly Glu Ser Phe
 20 25 30

Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu
 35 40 45

Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu
 50 55 60

Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val
 65 70 75 80

Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala
 85 90 95

10295.204.ST25.txt

Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala
 100 105 110
 Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser
 115 120 125
 Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg
 130 135 140
 Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu
 145 150 155 160
 Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His
 165 170 175
 Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp
 180 185 190
 Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp
 195 200 205
 Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe
 210 215 220
 Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu
 225 230 235 240
 Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val
 245 250 255
 Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr Pro Thr Thr Leu Phe
 260 265 270
 His His Val Gln His Ala Glu Glu Tyr Arg Gln Thr Pro Ala Val Gly
 275 280 285
 Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile Leu Ala Ser Thr Phe
 290 295 300
 Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His Pro Ser Leu Leu Pro
 305 310 315 320
 Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp Thr His Ile Pro Ile
 325 330 335
 Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val Glu Phe Leu Arg Met
 340 345 350
 Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr Ala Met Gly Leu Ile
 355 360 365

10295.204.ST25.txt

Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn Val Gly Leu Phe Ser
 370 375 380

Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala Ile Gly Ala Tyr Thr
 385 390 395 400

Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys Met Val Lys Leu Phe
 405 410 415

Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu Gly Phe Val Ile Gly
 420 425 430

Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile Arg Ser Leu Arg Thr
 435 440 445

Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly Lys Ala Phe Trp His
 450 455 460

Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys Val Arg Pro Ser Ile
 465 470 475 480

Val His Pro Arg Asn Arg Ser Arg Gln Pro
 485 490

<210> 88
 <211> 1567
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1064)

<400> 88
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 cagccgcttt acgagctgtc tgtcacagca aagccgaaga acattccgca gacgatcgag 180
 gttgatattt ccagtctcga agtcaatgat gttctaaccg tcggcgatat tccgaccaa 240
 ggcgattatt catacaacca tgagcctgat gaagttgttg catccattct tcctcctcaa 300
 aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc 360
 actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt 420
 tgtgctagaa tgaggggaaa ttaggatgct cccctcagt atgctgaggc agggttttgc 480
 ttaagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt 533
 Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly
 1 5 10
 aaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac 581
 Lys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp
 15 20 25

10295.204.ST25.txt

gag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac Glu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn 30 35 40	629
gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val 45 50 55	677
aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu 60 65 70 75	725
ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp 80 85 90	773
gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser 95 100 105	821
gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca Ala Gly Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr 110 115 120	869
agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly 125 130 135	917
atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu 140 145 150 155	965
ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala 160 165 170	1013
tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys 175 180 185	1061
gta taaggcaaaa gggaacggaa catactagtc ttaaaaagac tcggtatgga Val	1114
ggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cggaagtctt	1174
gaccattctt atgtaaacag tgaacagtta ggctttaacc acttaacaaa tgatgaaaga	1234
aacgatatga tttcttatat ggataatggg gatttacacg tgaagacgat atgtgaagat	1294
tgtcaagaag cgcttgagcg aaacccggat tatcaccaat atcattcatt tattcaatag	1354
atagctttgg tgtagagact agaccaaagc atttttctat ttgaggaaga gaggaggggc	1414
tcatttgaac aatattcaat cctatataac aaaaagcgat gatttttaaatt ccatcgtcaa	1474
cggcttgaac gaagggctga aggaacagct gcttgcgggg ctctccggat ctgcccggtc	1534
gttattttaca gccgctctta caaaagaaac gag	1567

<210> 89
 <211> 188
 <212> PRT
 <213> Bacillus licheniformis
 <400> 89

10295.204.ST25.txt

Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly Lys Thr Tyr Glu Asn
 1 5 10 15

Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu
 20 25 30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile
 35 40 45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr
 50 55 60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu
 65 70 75 80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro
 85 90 95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn
 100 105 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg
 115 120 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp
 130 135 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu
 145 150 155 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro
 165 170 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val
 180 185

<210> 90
 <211> 2097
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1598)

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 gtccgccttt caaaagccgg tcattttgct ggcagggggg cttgaccgag gaaatgaatt 180
 tgatgaacta aagccgcata tgtcttttgt aaaagcgggtg atcacttttcg gcgagaccgc 240
 gccgaagttt gagaagctgg ccgaagaaat gggaatacaa cagggttaaac gtgtcgataa 300

10295.204.ST25.txt

tgttgaacaa gcagcaactg cggcgttcag cctgtcagac gaaggagatg tcattcttct 360
 gtccccggcc tgcgcaagct gggatcagta caaaacattt gaagaacgtg gtgacatgtt 420
 tgtaaacgcc gtgcatatgc ttaaataagg gcttgtctcg taaagatagc cctaagaatt 480
 agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg 533
 Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu 10
 1
 ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta 581
 Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val 25
 15
 tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt 629
 Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe 40
 30
 ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc 677
 Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala 55
 45
 atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg 725
 Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala 75
 60
 aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt 773
 Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val 90
 80
 ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc 821
 Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val 105
 95
 ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc 869
 Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile 120
 110
 gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg 917
 Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser 135
 125
 ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt 965
 Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe 155
 140
 ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc 1013
 Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val 170
 160
 ggc aca tgc atc att atg atc ttt gtc gcg ggg gcg aga att tcg cac 1061
 Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His 185
 175
 ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg 1109
 Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val 200
 190
 ctg tcg gcg ccg tac cgg atc aaa agg atc act tca tac ttg aac cct 1157
 Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro 215
 205
 tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat 1205
 Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr 235
 220
 gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc ggc cag agc agg 1253
 225

10295.204.ST25.txt

Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Gln Ser Arg
 240 245 250

caa aag ttt ttc tat ctg cct gag ccg cag aca gat ttt att ttt gcg 1301
 Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
 255 260 265

att tta tca gag gag ctc ggc ttt atc ggc gga tcg ctg att ctt ttg 1349
 Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
 270 275 280

ctc ttc agc gtt cta tta tgg aga ggc atc aga atc gcg ctc ggt gcg 1397
 Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
 285 290 295

ccc gat tta tac ggc agt ttt gtc gcc gtc ggc gtc att tcg atg ata 1445
 Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
 300 305 310 315

gcg att cag gtt atg atc aat atc gga gtc gtg act ggt ttg att cct 1493
 Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
 320 325 330

gtt aca ggc att acg ctt ccg ttt tta agc tat ggc ggt tca tca ctg 1541
 Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
 335 340 345

acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg aat gtc agc agg tat 1589
 Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
 350 355 360

tct aga tac tagattttgg cgataaccct gttgcgagat agcagggtta 1638
 Ser Arg Tyr
 365

tcggcgtgta cataaggatt aagggggaga acagatgcgg attgttggtta gcggaggcgg 1698

aacgggcggc catattttacc ccgcccttgc gttttattaaa gaagtgaac ggcatcacga 1758

agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata tcgtcgagcg 1818

ggaaggggatc cttttcaaag cgattgaaat tacgggtttt aaaagaaaac tttcatttga 1878

aaacgtcaaaa accgtcatgc gctttttttaa ggggtgtaaaa gaatgcaaag aagaattaaa 1938

acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc ccgtcgtata 1998

cgccgcttca aaactgggga ttccgacgat tatccacgaa caaacagcc ttcccggact 2058

caccaataag tttttatcca aatatgttga taaggtagc 2097

<210> 91

<211> 366

<212> PRT

<213> Bacillus licheniformis

<400> 91

Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu Leu Val Ile Ile Thr
 1 5 10 15

Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val Tyr Ser Ala Ser Ala
 20 25 30

Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg

10295.204.ST25.txt
45

35

40

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met
 50 55 60
 Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile
 65 70 75 80
 Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met
 85 90 95
 Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile
 100 105 110
 Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys
 115 120 125
 Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe
 130 135 140
 Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met
 145 150 155 160
 Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile
 165 170 175
 Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly
 180 185 190
 Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr
 195 200 205
 Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu
 210 215 220
 Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly
 225 230 235 240
 Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr
 245 250 255
 Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu
 260 265 270
 Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Leu Phe Ser Val Leu
 275 280 285
 Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly
 290 295 300
 Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met
 Page 128

10295.204.ST25.txt

305 310 315 320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr
 325 330 335

Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu Thr Leu Met Leu Met
 340 345 350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr
 355 360 365

<210> 92
 <211> 1882
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1397)

<400> 92
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 atcggttcat acatcataac aaaaggggggt ttttttcatg aggcctgagtg aacttttcggg 120
 aaaagaaatc gttgatgtta agcggggccga acggctcggc gtactggggc agacggacct 180
 tgagatcaat gaggcaggacg gtcagattac cgctcttatac atcccttctg ttaaattggtt 240
 cggactagga agaaaacagg ggaatgacat taagggtgccc tggctcgcaaa ttcaaaaaat 300
 cggctcggat atgatcattt tggatgttcc ggaaagcagc gtgacaaaag aggagtaagc 360
 aagggtgaaa cccgcccgtc ccatgggggc gggctttttg tttttctgga tttcaattca 420
 ccgctatttc ctttttgtca tatgatgaaa ttagcttatg aattagatcc ttgtcaaaaa 480
 agaagggtgaa tgtagagacc atg tta acc gga ttg acg att gca atc atc ggc 533
 Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly
 1 5 10
 ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat 581
 Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp
 15 20 25
 gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc 629
 Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr
 30 35 40
 gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac 677
 Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp
 45 50 55
 agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg 725
 Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala
 60 65 70 75
 act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa 773
 Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu
 80 85 90
 aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat 821
 Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr

10295.204.ST25.txt

100

105

95
 tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt 869
 Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe
 110 115 120
 gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt 917
 Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly
 125 130 135
 gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg 965
 Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser
 140 145 150 155
 aat gta atg gtt ctc ggg ctg ggg cgg acg gga atg agc atc agc cgg 1013
 Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg
 160 165 170
 acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc 1061
 Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser
 175 180 185
 gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca 1109
 Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr
 190 195 200
 aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc 1157
 Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr
 205 210 215
 att cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc 1205
 Ile Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro
 220 225 230 235
 aga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt 1253
 Arg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe
 240 245 250
 gat ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt 1301
 Asp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu
 255 260 265
 ccc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt 1349
 Pro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val
 270 275 280
 ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca 1397
 Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
 285 290 295
 taatgtcgat caaaggaaaa agaatcggat ttggcctaac gggttcacat tgtacgtatg 1457
 atgccggtttt tccgcagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggctcg 1517
 tgacgcatac tgtcaagtcg acggatacac gctttggaga aggggaagaa tgggtcagaa 1577
 gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg 1637
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 agcttgcaaa cgcccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa 1757
 actcccgtcc cgtcgtcctc ggcatttcaa cgaatgacgc gctcggcttg aacggcgta 1817
 acttgatgag gctgatggcg gcaaaaaatg ttacttttat tccgttcggc caggatgacc 1877
 1882
 cttac

10295.204.ST25.txt

<210> 93
 <211> 299
 <212> PRT
 <213> Bacillus licheniformis

<400> 93

Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly Gly Asp Ala Arg Gln
 1 5 10 15

Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp Ala Lys Val Phe Leu
 20 25 30

Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu
 35 40 45

Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro
 50 55 60

Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn
 65 70 75 80

Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His
 85 90 95

Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala
 100 105 110

Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile
 115 120 125

Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala
 130 135 140

Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu
 145 150 155 160

Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu
 165 170 175

Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg
 180 185 190

Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu
 195 200 205

His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile
 210 215 220

Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu
 225 230 235 240

10295.204.ST25.txt
 Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Asp Phe Ala Glu Lys
 245 250 255

Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala
 260 265 270

Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu
 275 280 285

Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
 290 295

<210> 94
 <211> 1588
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1088)

<400> 94
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 tcggcgctcg gcgcacgcgt aaaagtcgga gctcgcgact ccgcccacct cgccagaatc 180
 atggagatgg gcctcactcc tttccacaca aacgaacttg cagagcatgt tgaaaatata 240
 gacatatgca tcaataccat tccaagcctg attctcgata aacatgtcct ctcacgaatg 300
 acaccagaaa cattaattct cgatttagca acccggtccg gaggcacaga ttttgatttt 360
 gccgaaaagc aaggcattaa agcgtgctt gctccaggac ttcccgggat cgtcgcgcct 420
 aaaacggcgg gacagatcat tgccaatggt ttgtgcaacc tttgtctga attaacaact 480
 gaccgaaagg ggctgtcata atg tcg atc aaa gga aaa aga atc gga ttt ggc 533
 Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly
 1 5 10
 cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa 581
 Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu
 15 20 25
 gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act 629
 Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr
 30 35 40
 gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga 677
 Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg
 45 50 55
 aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa 725
 Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys
 60 65 70 75
 gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg 773
 Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala
 80 85 90
 cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac 821
 Page 132

10295.204.ST25.txt

Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp
 95 100 105

agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc 869
 Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro
 110 115 120

gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc 917
 Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val
 125 130 135

aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc 965
 Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe
 140 145 150 155

ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg 1013
 Gly Gln Asp Asp Pro Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met
 160 165 170

gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata 1061
 Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile
 175 180 185

cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag 1108
 Gln Pro Ile Leu Val His Asn Asp Gln
 190 195

atgtaacaaa aaatatcaat caccacggca cacatctatg ttaaaataaa atgtaaaatg 1168

catagtcaac caatcgttta cgacgattaa ggtggaagga gttttacaat tgggcagagg 1228

attacatgta gcagtagttg gtgcgacagg cgctgtagga cagcaaattgt taaaaacact 1288

agaagacagg aattttgaac tggataaaact gactttatta tcctcaaaac gttcagcagg 1348

tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgtc ctgagagctt 1408

tgaaggcgtc aacatcgcg ttttcagcgc cgggggaagc gtttcgcagg cgcttgctca 1468

cgaggctgtc aaacgcgggg cgatcgtc tgcataatag agcgcgttcc ggatggacca 1528

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<210> 95

<211> 196

<212> PRT

<213> Bacillus licheniformis

<400> 95

Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly Leu Thr Gly Ser His
 1 5 10 15

Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys
 20 25 30

Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp
 35 40 45

Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg Arg Ile Glu Glu Leu
 50 55 60

Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly
 Page 133

10295.204.ST25.txt
75

65 70 80

Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn
85 90 95

Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met
100 105 110

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile
115 120 125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu
130 135 140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro
145 150 155 160

Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met Asp Leu Leu Val Pro
165 170 175

Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile Gln Pro Ile Leu Val
180 185 190

His Asn Asp Gln
195

<210> 96
<211> 2167
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1871)

<400> 96
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aggaatttct gaagctgcag agaaaaatgg cattccgtgt acattcaaca gggcggggtc 120
tatgatcggc tttttcttca caaatggacc ggtcatcaat tatgatacag cgaaacagtc 180
tgacctcgga ctgtttgccg aatattataa aggaatggcc gatgaaggcg tgtttctgcc 240
gccttcacag tttgaagggc tgttcttgtc aaccgctcat acggatgacg acattgagca 300
tacgattaaa gctgctgaac gcgtattcga aagaatcagc cgctccagat aaagaaaagg 360
gctgccggac attgccggcg gctctttttt gcatggtgcc gaaaacggct gctgattttt 420
ctgttcatat tctgcctgct tttcacatac atctttactg acatctaatt ttaaaaatta 480
ggtgaaggga ggatatcagt ttg ccg caa aac aat cgt ttg caa ttt tct gta 533
Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val 10
1

gaa gag tca atc tgt ttt caa aaa gga cag gaa gta tcc gaa tta tta 581
Glu Glu Ser Ile Cys Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu

10295.204.ST25.txt

15															20										25										
tcg	att	tca	ttg	gat	cct	gac	att	acc	gtt	cag	gaa	gta	aat	gat	tat	629																			
Ser	Ile	Ser	Leu	Asp	Pro	Asp	Ile	Thr	Val	Gln	Glu	Val	Asn	Asp	Tyr																				
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gta	tcc	ata	cga	ggg	tca	tta	gag	ctg	aca	ggc	gaa	tac	aac	ata	gat	677																			
Val	Ser	Ile	Arg	Gly	Ser	Leu	Glu	Leu	Thr	Gly	Glu	Tyr	Asn	Ile	Asp																				
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caa	acc	cgg	gag	tat	gca	gag	ctg	cct	gcg	aca	agc	cga	ttt	gta	gaa	725																			
Gln	Thr	Arg	Glu	Tyr	Ala	Glu	Leu	Pro	Ala	Thr	Ser	Arg	Phe	Val	Glu																				
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gat	gta	aag	ctg	aaa	ggg	gac	ggc	agc	gca	gag	ctg	acg	cat	tgt	ttc	773																			
Asp	Val	Lys	Leu	Lys	Gly	Asp	Gly	Ser	Ala	Glu	Leu	Thr	His	Cys	Phe																				
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cca	gtg	gat	atc	acc	atc	ccg	aaa	gac	aaa	gtc	aat	cat	tta	aac	gac	821																			
Pro	Val	Asp	Ile	Thr	Ile	Pro	Lys	Asp	Lys	Val	Asn	His	Leu	Asn	Asp																				
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gta	ttt	gtt	ttt	att	gac	gct	ttc	gat	tat	cag	ctg	aca	gat	gcg	agg	869																			
Val	Phe	Val	Phe	Ile	Asp	Ala	Phe	Asp	Tyr	Gln	Leu	Thr	Asp	Ala	Arg																				
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atg	ctg	acg	att	cag	gct	gat	ttg	gcg	att	gaa	ggc	ctc	ttg	aat	gtg	917																			
Met	Leu	Thr	Ile	Gln	Ala	Asp	Leu	Ala	Ile	Glu	Gly	Leu	Leu	Asn	Val																				
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agc	ggt	gaa	gcg	ggt	gaa	gaa	gaa	ccg	cgc	act	atg	cct	gcg	gcc	gtc	965																			
Ser	Gly	Glu	Ala	Gly	Glu	Glu	Glu	Pro	Arg	Thr	Met	Pro	Ala	Ala	Val																				
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cat	ccg	gaa	gag	gag	ctc	gaa	cct	gcc	tac	aga	tca	cct	tca	aac	gac	1013																			
His	Pro	Glu	Glu	Glu	Leu	Glu	Pro	Ala	Tyr	Arg	Ser	Pro	Ser	Asn	Asp																				
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gaa	gat	cag	ggt	gaa	gag	aaa	gaa	tat	ttg	atc	cag	ctt	gac	aga	cct	1061																			
Glu	Asp	Gln	Gly	Glu	Glu	Lys	Glu	Tyr	Leu	Ile	Gln	Leu	Asp	Arg	Pro																				
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tac	gaa	gag	cag	gac	gaa	gaa	cag	gcg	gaa	gaa	cat	gat	acc	ggt	gag	1109																			
Tyr	Glu	Glu	Gln	Asp	Glu	Glu	Gln	Ala	Glu	Glu	His	Asp	Thr	Gly	Glu																				
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gaa	acg	gtt	ccg	att	tac	cag	tcg	ttt	ctc	gga	aac	gac	aca	gag	gaa	1157																			
Glu	Thr	Val	Pro	Ile	Tyr	Gln	Ser	Phe	Leu	Gly	Asn	Asp	Thr	Glu	Glu																				
															205											210	215								
gct	aaa	ccg	ttt	ttt	aca	gcg	tct	ttg	tcg	gcg	gca	gag	cgt	acg	aag	1205																			
Ala	Lys	Pro	Phe	Phe	Thr	Ala	Ser	Leu	Ser	Ala	Ala	Glu	Arg	Thr	Lys																				
															220											225	230	235							
cgc	gaa	ata	gaa	aat	caa	aaa	gaa	gcc	tct	ctt	gaa	cag	ccg	gaa	gaa	1253																			
Arg	Glu	Ile	Glu	Asn	Gln	Lys	Glu	Ala	Ser	Leu	Glu	Gln	Pro	Glu	Glu																				
															240											245	250								
gaa	tat	aag	ctg	aaa	aga	gag	aaa	gtg	gaa	gag	gaa	ccg	gaa	gaa	tat	1301																			
Glu	Tyr	Lys	Leu	Lys	Arg	Glu	Lys	Val	Glu	Glu	Glu	Pro	Glu	Glu	Tyr																				
															255											260	265								
gag	ctg	aaa	aga	gag	aaa	gtg	gaa	gag	gaa	ccg	gaa	gaa	tat	gag	ctg	1349																			
Glu	Leu	Lys	Arg	Glu	Lys	Val	Glu	Glu	Glu	Pro	Glu	Glu	Tyr	Glu	Leu																				
															270											275	280								
aaa	aga	gaa	gaa	gcg	gaa	gaa	gag	ccg	gag	ctg	tcg	cac	agc	tct	tat	1397																			
Lys	Arg	Glu	Glu	Ala	Glu	Glu	Glu	Pro	Glu	Leu	Ser	His	Ser	Ser	Tyr																				

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10295.204.ST25.txt
295

285 290 1445
 caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct
 Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro
 300 305 310 315

1493
 ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt
 Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val
 320 325 330

1541
 gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg
 Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly
 335 340 345

1589
 cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc
 His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro
 350 355 360

1637
 gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca
 Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser
 365 370 375

1685
 gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag
 Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys
 380 385 390 395

1733
 cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa
 Gln Gly Glu Glu Glu Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln
 400 405 410

1781
 aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag
 Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln
 415 420 425

1829
 cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag
 Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu
 430 435 440

1871
 gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc
 Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala
 445 450 455

1931
 taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaattgag

1991
 tacggtctta cgcctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgtatacg

2051
 gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa

2111
 cagatgatca tgctggagga aaaaggctac aggcagttcg ttctgtctta tcgaaaccgc

2167
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 <213> Bacillus licheniformis

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 20 25 30

10295.204.ST25.txt

Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly
 35 40 45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr
 50 55 60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys
 65 70 75 80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr
 85 90 95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile
 100 105 110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln
 115 120 125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly
 130 135 140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu
 145 150 155 160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu
 165 170 175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp
 180 185 190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile
 195 200 205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe
 210 215 220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn
 225 230 235 240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Glu Tyr Lys Leu Lys
 245 250 255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu
 260 265 270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala
 275 280 285

Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu
 290 295 300

10295.204.ST25.txt

Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp
 305 310 315 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu
 325 330 335

Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly His Thr Ile Glu Ile
 340 345 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp
 355 360 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp
 370 375 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu
 385 390 395 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp
 405 410 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met
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Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr
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Ile Pro Asp Tyr Gln Asn Ser His Ala
 450 455

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 <211> 1955
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 aaaaaggcga atttcatttc cttcaaatac aaaagacttt ggtgaagatc ccgctgtgaa 180
 acaggggaga gccgagcagc gcctgcagca catcttcaga cagattggct ccattccccg 240
 aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac 300
 caaacaggat gaaaaaattg gtttgtccgc acagcttacc tgaatacaat aaaaaataaa 360
 gtatttctcg ggaaagcgca ggtttcaaca agacctgccc cgttcttgtc aaaaagcatt 420
 ggattgtgca gtcattgtgg cgtctgtcac ggcataagcg cgccatgaat aggatataaa 480
 gagagaatgg tgaggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac 533
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10295.204.ST25.txt

Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn
1 5 10

gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat	581
Gly Gln Ile Asn Ile Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn	
15 20 25	
tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc	629
Ser Glu Ala Glu Ala Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala	
30 35 40	
aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc	677
Lys His Ser Ile Leu Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val	
45 50 55	
gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att	725
Gly Met Glu Glu Met Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile	
60 65 70 75	
ttc gtt aat aaa aag cgc gaa gaa caa ggc ctt aag gcc gga aaa cag	773
Phe Val Asn Lys Lys Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln	
80 85 90	
gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc	821
Ala Leu His Met Met Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr	
95 100 105	
gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca	869
Val Ala Arg Leu Ile Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser	
110 115 120	
aaa ggc cat ctg atc gag gcg gag cgc gcc gat ctc gtc ggt gag tac	917
Lys Gly His Leu Ile Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr	
125 130 135	
atc ggc cat acg gcg caa aaa acg agg gat tta atc aaa aaa gcg atg	965
Ile Gly His Thr Ala Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met	
140 145 150 155	
ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga	1013
Gly Gly Ile Leu Phe Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly	
160 165 170	
gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg	1061
Glu Lys Asp Phe Gly Lys Glu Ala Ile Asp Thr Leu Val Lys His Met	
175 180 185	
gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg	1109
Glu Asp Lys Arg Asn Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg	
190 195 200	
gaa atg gat cat ttt ctt tca tta aac ccg ggc ctt cag tca agg ttt	1157
Glu Met Asp His Phe Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe	
205 210 215	
ccg atc agc atc gat ttt ccc gat tac tca gtc agc cag ctg atg gac	1205
Pro Ile Ser Ile Asp Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp	
220 225 230 235	
att gca aaa cgg atg atg gcg gaa agg gaa tat cag ttc agc cct gag	1253
Ile Ala Lys Arg Met Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu	
240 245 250	
gct gaa tgg aag ctg aaa gac cat ctg atg gcc gtc aaa agt acg gtc	1301
Ala Glu Trp Lys Leu Lys Asp His Leu Met Ala Val Lys Ser Thr Val	
255 260 265	
agc ccc gcg aag ttc agc aat ggc cgt ttc gtc cgc aac ctg atc gaa	1349

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10295.204.ST25.txt

Ser Pro Ala Lys Phe Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu
 270 275 280

aaa tcc atc cgg tcg cag gcg atg aga ctg ctg atg gga gac tgc tac 1397
 Lys Ser Ile Arg Ser Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr
 285 290 295

tta aag aat gac ttg ata acc atc aaa agc cag gat ctc gac ttg aag 1445
 Leu Lys Asn Asp Leu Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys
 300 305 310 315

gaa gac gcg ccg cac gta taatggcgcg ttcttttttt attttcgagg 1493
 Glu Asp Ala Pro His Val

atttctggca accgctccct tcgtttgtta tgatagtact gcttattgac taacgttaag 1553
 aaaggaacat gatacttga acgaacagga agtcatgaaa gagaaagcca tattagtcgg 1613
 atgccagctt ccgcacgtgt ctgatgagcg tttttcatac tcgatggaag agctcgccgc 1673
 gctgacgaaa acggccgacg gaacggttgt ttccacggtc acgcagaagc ggaaccgtgt 1733
 ggatgctgct acatatatcg gaaaaggaaa agtagatgaa ttggcggtgc tctgtgaaga 1793
 gctgtcgccc gatgttttaa tttttaatga tgaattgtcg ccgagtcagc tgaaagcgct 1853
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 <213> Bacillus licheniformis

<400> 99

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 20 25 30

Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu
 35 40 45

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met
 50 55 60

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys
 65 70 75 80

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met
 85 90 95

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile
 100 105 110

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile

10295.204.ST25.txt

115

120

125

Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala
 130 135 140

Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe
 145 150 155 160

Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly
 165 170 175

Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn
 180 185 190

Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe
 195 200 205

Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp
 210 215 220

Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met
 225 230 235 240

Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu
 245 250 255

Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe
 260 265 270

Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser
 275 280 285

Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu
 290 295 300

Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys Glu Asp Ala Pro His
 305 310 315 320

val

<210> 100
 <211> 2082
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1607)

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60

10295.204.ST25.TXT

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tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaattg	240
tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg	300
aggaaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa	360
ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga	420
ataaaatcaa gccgtgccaa ttttagcggca ggcatacataa cttatttttgg aactttttga	480
atg atc ccg tta gtc aat tta aaa cgt caa ttt Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe 1 5 10	533
caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp 15 20 25	581
agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg 30 35 40	629
ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly 45 50 55	677
acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly 60 65 70 75	725
gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala 80 85 90	773
gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu 95 100 105	821
aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala 110 115 120	869
act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met 125 130 135	917
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu 140 145 150 155	965
gat gcc tgc caa gcg ttc ggc gca tgc tat aaa gag cgg cct gtc ggc Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly 160 165 170	1013
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu 175 180 185	1061
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala 190 195 200	1109
gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr	1157

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215

205 -210

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Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala	
220 225 230 235	
gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa	1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln	
240 245 250	
aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag	1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu	
255 260 265	
cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat	1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His	
270 275 280	
ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg	1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu	
285 290 295	
aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat	1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His	
300 305 310 315	
ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct	1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro	
320 325 330	
ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct	1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro	
335 340 345	
ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa	1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys	
350 355 360	
aaa gga gga ggg gaa aag tgacgggttca ttttggttta atcggctgcg	1637
Lys Gly Gly Gly Glu Lys	
365	
gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg	1697
ccgtcagtgaa tttgcaggaa gaaagaatga aggaagcggg agaatactat gcttcctcgg	1757
ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta	1817
aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg	1877
cgctgctggc aggcaagcac gtcacgctcg aaaaaccgat gaccttgatc ttacgggatg	1937
ccgatgagct tatagaactg gcggagcaga acgggctgaa gtcacatggc tgccaccaga	1997
tgcgccaccg gccgatcatg aaaaaactga aggaacgat tgaggaagga aagctgggaa	2057
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<210> 101
 <211> 369
 <212> PRT
 <213> Bacillus licheniformis

<400> 101

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WO 03/087148

10295.204.ST25.txt

Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile
 20 25 30
 Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
 35 40 45
 Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
 50 55 60
 Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
 65 70 75 80
 Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
 85 90 95
 Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
 100 105 110
 Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
 115 120 125
 Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
 130 135 140
 Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
 145 150 155 160
 Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
 165 170 175
 Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
 180 185 190
 Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
 195 200 205
 Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
 210 215 220
 Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
 225 230 235 240
 Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
 245 250 255
 Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
 260 265 270
 Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
 275 280 285

WO 03/087148

10295.204.ST25.txt

ctg cag gga gac att ttg gat ttg aac gcg ctt aaa aag gcg atc cag Leu Gln Gly Asp Ile Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln 60 65 70 75	725
ggg gcc agc cac att gtc cac gcc gcc ggc atc gct ggg att gac acg Gly Ala Ser His Ile Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr 80 85 90	773
gtc att caa aac ccg gtt aaa acg atg cag gtc aac atg atc ggt tca Val Ile Gln Asn Pro Val Lys Thr Met Gln Val Asn Met Ile Gly Ser 95 100 105	821
gcc aat ctg ctt gaa gcg gct gcc ggt tta acc gaa tgc aaa agg gtt Ala Asn Leu Leu Glu Ala Ala Gly Leu Thr Glu Cys Lys Arg Val 110 115 120	869
gtc tgt ttc agt aca agc gaa gtg ttc ggc caa atc gct ttc aga gcg Val Cys Phe Ser Thr Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala 125 130 135	917
cgc gag acc agt cat act gtt tta gga gcg gtg gga gaa gcc cgc tgg Arg Glu Thr Ser His Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp 140 145 150 155	965
aca tat gct gtc agc aaa ctc gcc gag gag cat atg gca tat gcc tat Thr Tyr Ala Val Ser Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr 160 165 170	1013
ttt aaa gaa ctt ggg ctt ccg acc gtc acc gtc cgc cct ttt aat gtt Phe Lys Glu Leu Gly Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val 175 180 185	1061
tat gga ccg gaa caa gtc ggc gaa ggc gcc atc aaa acg atg gtt cac Tyr Gly Pro Glu Gln Val Gly Glu Gly Ala Ile Lys Thr Met Val His 190 195 200	1109
aga gct ctg tta gat gag ccg atc tat att cac ggc gat gga acg caa Arg Ala Leu Leu Asp Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln 205 210 215	1157
atc cgg gcc tgg tgt tac gta gat gac atg atc gac gga att ttg cgt Ile Arg Ala Trp Cys Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg 220 225 230 235	1205
tgt ttg acg atg aag gaa gcc atc gga gag tct ttc aac atc ggc aat Cys Leu Thr Met Lys Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn 240 245 250	1253
gaa cgc act gtg atc acc gta tac gga ttg gca agc acg att atc aga Glu Arg Thr Val Ile Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg 255 260 265	1301
gtt ctc gga tca aaa tca caa atc ttc ttt ggg gag aaa aaa gaa gcc Val Leu Gly Ser Lys Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala 270 275 280	1349
gat att gaa ctg cgc atc cct cag gtc aat aaa gca aaa gag atg ctc Asp Ile Glu Leu Arg Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu 285 290 295	1397
ggt ttc agc gct aaa gtt gat ctg gaa gaa ggc atc aga aga aca gct Gly Phe Ser Ala Lys Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala 300 305 310 315	1445
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10295.204.ST25.txt

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ggagataacg tttatatcgg ccatgacacg attttaaaag gctattataa gcatgacctg 1672
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gatcctgata aaccgcagac taccattttg ttttcgccgc ttacattcgc tcctattcat 1852
attgaagaaa actgcaacat cgggatcggg gcgtctatcc tagcaggcgt tacgataggc 1912
gcccactcca aaatcggagc aaatgccgtc gtcaatcgca atattccccc gtacagcata 1972
gca 1975

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<210> 103
<211> 324
<212> PRT
<213> Bacillus licheniformis

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<400> 103

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1          5          10          15

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Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly Lys Leu Ile Glu Arg
          20          25          30

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Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg Asp Ser Leu Arg Tyr
          35          40          45

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Lys Pro Tyr Arg Asp His Pro His Leu Lys Val Leu Gln Gly Asp Ile
          50          55          60

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Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln Gly Ala Ser His Ile
          65          70          75          80

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Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr Val Ile Gln Asn Pro
          85          90          95

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Val Lys Thr Met Gln Val Asn Met Ile Gly Ser Ala Asn Leu Leu Glu
          100          105          110

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Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val Val Cys Phe Ser Thr
          115          120          125

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Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala Arg Glu Thr Ser His
          130          135          140

```

```

Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp Thr Tyr Ala Val Ser
          145          150          155          160

```

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Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr Phe Lys Glu Leu Gly

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10295.204.ST25.txt
170

175

165

Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val Tyr Gly Pro Glu Gln
180 185 190

Val Gly Glu Gly Ala Ile Lys Thr Met Val His Arg Ala Leu Leu Asp
195 200 205

Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln Ile Arg Ala Trp Cys
210 215 220

Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg Cys Leu Thr Met Lys
225 230 235 240

Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn Glu Arg Thr Val Ile
245 250 255

Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg Val Leu Gly Ser Lys
260 265 270

Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala Asp Ile Glu Leu Arg
275 280 285

Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu Gly Phe Ser Ala Lys
290 295 300

Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala Glu Ser Ile Lys Lys
305 310 315 320

Asn Leu Asp Gln

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<211> 1213
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<213> Bacillus licheniformis

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tgcgcccttt aatcggcatg gataagacgg aaatcatcga aaaagcgaag gaaatcgata 180
cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg ctttctgcgc 240
cgaaaacgcg tccgaaaaaa gagaaaatcg aacactttga aagctacaca gatttcgaac 300
cgcttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcgga 360
cgaaagatca atttgccgat tttttctaaa ggaatattca atcaaacatc tttgtctgtt 420

tttgcataca attaccaaac attctttgta tgaagtcatg tgtttttaca caatctatac	480
tcacaaggag gtgagaacac atg gct caa aac aac aga caa agc agt tct aac	533
Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn	
1 5 10	
caa cta ttg gtt cct ggt gct gct caa gct atc gac caa atg aaa ttc	581
Gln Leu Leu Val Pro Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe	
15 20 25	
gaa atc gct tct gaa ttt ggc gtt aac ctt gga gca gaa act act tct	629
Glu Ile Ala Ser Glu Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser	
30 35 40	
cgt gca aac ggt tca gtt gga gga gaa atc act aag cgt tta gtt tct	677
Arg Ala Asn Gly Ser Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser	
45 50 55	
ttc gct caa cag caa atg ggt gga aca caa caa taattaaaat taaaaagcaa	730
Phe Ala Gln Gln Gln Met Gly Gly Thr Gln Gln	
60 65 70	
tggataatgg gtgggggttta atccccactc ttttttatgt tctgcaaaat aggcatttcg	790
gaatacaatt gtatgaaagg attatgtata ataaaaagat ggcacaagac aaggagatgg	850
aagggttgag aagagaagat ttgattgcgc cggagaagta taatgcgggt gatgaaattg	910
aaaaatttaa atcttcccgc gataagaccg cattgatctg ggaagatgaa tcagggcgctc	970
aagtgtcatg gtcctatgaa aaattgattg aaaaggctta caaaatcggc agcatattga	1030
cccgttctgg actgaaaaaa ggtgacaagc ttatcgtgat gatgccgcgg ataccggaaa	1090
cgtatgccgt gtacatggcc attttaaaag ctggaatggt ggtcatccca tgttccgaaa	1150
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tat	1213

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<210> 105
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<212> PRT
<213> Bacillus licheniformis
<400> 105
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Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn Gln Leu Leu Val Pro
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Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe Glu Ile Ala Ser Glu
20 25 30

Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser Arg Ala Asn Gly Ser
35 40 45

val gly gly glu ile thr lys arg leu val ser phe ala gln gln gln
50 55 60

Met Gly Gly Thr Gln Gln
65 70

10295.204.ST25.txt

<210> 106
 <211> 1196
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(695)

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 ggccgcttgaa aaaatcgtca ttgagcagac tggacagctc cgcgattttt ataaagatct 240
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 cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtcttct taaaatatga 360
 aatgaaataa tcgccgaccg gcgcgcctgg cttgccaat gccaggcggt tttttgccct 420
 tcaacaattg ccagcataaa aagcctcagt ccaaatacaa ctaaacaagc agtaccaatt 480
 gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg 533
 Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly
 1 5 10
 gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc 581
 Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe
 15 20 25
 ggc gtc cag ctc ggc tgc gac tgc gtc gct cgc tca aac gga tct gta 629
 Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val
 30 35 40
 ggc ggc gaa atg aca aaa cga ctt gta cag cag gca caa gct caa ttg 677
 Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu
 45 50 55
 aat ggc cat aat gac aaa taaataccct atggattatt cgccgggccc 725
 Asn Gly His Asn Asp Lys
 60 65
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 aagtgattta gagctctctt gatttgaacc ggaaccgctt tttggcgctt cttcctccgt 845
 ctgctgaccg tctttgtcat tatggttatg ttcctgaggg tttttggtat taggggaatt 905
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<210> 107
 <211> 65
 <212> PRT
 <213> Bacillus licheniformis

10295.204.ST25.txt

<400> 107

Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly Ala Glu Gln Val Leu
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Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly
 20 25 30

Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr
 35 40 45

Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp
 50 55 60

Lys
 65

<210> 108

<211> 2279

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1463)

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ccggcttgca ccgaatgaca gcgattatct tttaatcaaa ccaaagcact cagcctttta 180

cggcactgct cttgaaacat tgctgcatga acttcatgtc gatcatttga tcatcactgg 240

gatcgcaggc aatatctgcg tattattttac ggcaaacgat gcttatatgc gggagtagca 300

gattacgatt ccgcgcgatt gcatcgctc aaacaatgaa aaagacaaca aatagcctt 360

gacgatgatg gaaaatgttc tgttcgccaa tatcacgacg gctaaggcga ttacctccga 420

aacttagagc atgaaacact tcctttcatc atatagtggg agcaatgaga aaggaggcgt 480

ttccattca gatttatgtc gtg aaa aga ggc gat acc ctt tac caa atc gcg 533
 Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala
 1 5 10

aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att 581
 Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile
 15 20 25

ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc 629
 Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile
 30 35 40

gcc ggc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc 677
 Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile
 45 50 55

gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc 725
 Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg

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10295.204.ST25.txt
70

75

60 773
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ile Gln Val Ser Ala Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro
80 85 90

821
cct cgg cca aga cgg aac att gaa aca aac gcc tat atc gaa cct cgg
Pro Arg Pro Arg Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg
95 100 105

869
gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg
Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser
110 115 120

917
cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cgg gac
Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp
125 130 135

965
ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac
Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp
140 145 150 155

1013
aga cat cgg act acg atg atg atg att gtc acc aat ctc gaa aat gaa
Arg His Arg Thr Thr Met Met Met Ile Val Thr Asn Leu Glu Asn Glu
160 165 170

1061
gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta
Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val
175 180 185

1109
aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt
Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly
190 195 200

1157
ttt aaa gac atc cat ttt gac ttc gaa tac tta agg ccc gaa gat aga
Phe Lys Asp Ile His Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg
205 210 215

1205
gaa gcc tat aat cag ttt tta ccg gat gcc ccg gcc cgc ttc agg cag
Glu Ala Tyr Asn Gln Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln
220 225 230 235

1253
gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat
Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp
240 245 250

1301
cag ccc gga caa tgg tat gaa gcc cat gat tac ccg gcc cac ggc gaa
Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu
255 260 265

1349
att gtc gat ttc gtc gtg ctg atg aca tat gag tgg ggc tac agc gga
Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly
270 275 280

1397
ggg ccc ccg atg gcg gta tcg ccg atc ggg ccc gtc ccg gac gtg atc
Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile
285 290 295

1445
gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag
Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln
300 305 310 315

1493
aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggacccc
Lys Leu Tyr Gly Tyr Asp
320

1553
gttggccaag accaatccgg ccccaacggg gggattgaga tcgcgagcga gaacaatgcg

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gcgatacagt acgatgaaac agctcaggct ccaaacttcc gctatacggg caatgccggc 1613
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 aagaaatcgt cgaagaaaac ctttttcttg ataaatttta tgatgaaaaa gatgaatgga 2033
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 ctttat 2279

<210> 109
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 <213> *Bacillus licheniformis*

<400> 109

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20 25 30

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35 40 45

Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn
50 55 60

Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala
65 70 75 80

Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg
85 90 95

Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser
100 105 110

Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr
115 120 125

Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu
130 135 140

WO 03/087148

10295.204.ST25.txt

Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr
 145 150 155 160

Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu
 165 170 175

Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu
 180 185 190

Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His
 195 200 205

Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln
 210 215 220

Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile
 225 230 235 240

Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp
 245 250 255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val
 260 265 270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala
 275 285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr
 290 295 300

Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr
 305 310 315 320

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<210> 110
 <211> 2011
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (252)..(1508)

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 aagaattatc cgcttcacgg ttctattcac cattccagct gtaaaaaacg gcgcatgatc 180
 cttctgcaac ggtcatagac atagcataaa accccctgtc acatacagag gaacaaaagg 240

10295.204.ST25.txt

aagtgtgccca g ttg ttt att tat aca gtc cag ccg gga gat tca cta ttt Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe 1 5 10	290
gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala 15 20 25	338
aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile 30 35 40 45	386
ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att Pro Leu Tyr Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile 50 55 60	434
gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro 65 70 75	482
tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro 80 85 90	530
gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg 95 100 105	578
aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala 110 115 120 125	626
acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu 130 135 140	674
agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg 145 150 155	722
gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser 160 165 170	770
ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg 175 180 185	818
ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly 190 195 200 205	866
gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe 210 215 220	914
tca ggt ttt ctc cgc ctg ttg aaa gag ccg ctg aag ccg tcc ggc tat Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr 225 230 235	962
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ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc Leu Lys Gly Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile 255 260 265	1058

10295.204.ST25.txt

ttc atc atg gca tac gac tgg cac cac ggg aca agc gag ccc ggc ccc 1106
 Phe Ile Met Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro 285
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 att gct ccg atc aat gaa gtc cgg caa aca att caa ttt gct ctc cgc 1154
 Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg 300
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 cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt ccg ctt tac ggc tat 1202
 His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr 315
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 aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc 1250
 Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala 330
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 aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca ccg att caa 1298
 Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln 345
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 tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag 1346
 Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln 365
 350
 ggc aga cgg cat gtc gta tgg ttt gaa gac gca cgc agc atc gga aaa 1394
 Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys 380
 370
 aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc ggc gtc tgg 1442
 Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp 395
 385
 cag ctc aca ctc agt ttt ccg caa gga aca tgg ctc ttg acc aaa ttc 1490
 Gln Leu Thr Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe 410
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 ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata 1538
 Phe Arg Val Arg Lys Val 415
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<210> 111
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 <212> PRT
 <213> Bacillus licheniformis

<400> 111

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10295.204.ST25.txt

Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala Asn Gly Leu
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 Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr
 35 40 45
 Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg
 50 55 60
 Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr
 65 70 75 80
 Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro
 85 90 95
 Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg
 100 105 110
 Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu
 115 120 125
 Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu
 130 135 140
 Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro
 145 150 155 160
 Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu
 165 170 175
 Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp
 180 185 190
 Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile
 195 200 205
 Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe
 210 215 220
 Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr
 225 230 235 240
 Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly
 245 250 255
 Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met
 260 265 270
 Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro
 275 280 285

10295.204.ST25.txt

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro
 290 300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr
 305 310 315 320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp
 325 330 335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr
 340 345 350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg
 355 360 365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln
 370 375 380

Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp Gln Leu Thr
 385 390 395 400

Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe Phe Arg Val
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Arg Lys Val

<210> 112
 <211> 2014
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (558)..(1511)

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 catggccgaa aaaatatagc attccccctt cgccccgtcc atggctgtgt acataccggc 180
 aagcggccct ttccctctgt acgggtcgat atcttccagc accgcttttt tcccagattc 240
 tataaaccgc tccgtcaagc ccggacggct caatatcagg acgtcgtctc ccagcgctg 300
 tttgcaccat tgataaagcg gcttgccttt ccagcgggca aacgccttcg gttccccaaa 360
 acggcgcgaa agccccctg.ataatatgac atgtatttct ttcatacggc tcaaccttcc 420
 ttcgcgtgtt cctgcctgcg aacatcatag caaaacttta gaaatccgaa caagtctgta 480
 aaatctcttt ttcaaaaggc atggcggggt tcatattatgc atattgtagt tgtaacattt 540
 ataggggggct ggtcacc atg aaa aaa aca tcg ggt tcg ctg cct tat ttt 590
 Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe

10295.204.ST25.txt

1

5

10

caa gat tta tca cag gaa aac ctt ttt tta aaa gct gag ctg gca aga Gln Asp Leu Ser 15 Gln Glu Asn Leu Phe 20 Leu Lys Ala Glu Leu 25 Ala Arg	638
tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa Ser His Gln Leu Ile His Glu Leu 35 Glu Ala Ser Tyr Phe 40 His Gln Lys	686
aat cat aag ctc agc cgg gaa aac gca gca atg aaa cag cag ctt cag Asn His Lys Leu Ser Arg Glu Asn 50 Ala Ala Met Lys 55 Gln Gln Leu Gln	734
cag ctg tca ttc gaa ctg gag cgg att tcg gca aac aag gaa gac aag Gln Leu Ser Phe Glu 65 Glu Arg Ile Ser 70 Ala Asn Lys Glu Asp Lys 75	782
tcg gcc gaa acg ctc aac cgg ata aaa agc gaa ttg ctg agt aaa atc Ser Ala Glu Thr 80 Asn Arg Ile Lys 85 Glu Leu Leu Ser Lys 90 Ile	830
gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa Val Val Leu Gln 95 Glu Leu Leu Gln Lys 100 Glu Thr Tyr Ala Arg Lys Gln 105	878
gag ata gaa gaa aag cac cgc ctt cat tta aca aat gta aaa gcc gaa Glu Ile Glu Glu Lys His Arg Leu 115 His Leu Thr Asn Val 120 Lys Ala Glu	926
gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat Glu Glu Lys Lys Ser Leu His 130 Ser Gln Ile Glu Tyr 135 Glu Lys Leu His	974
gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa Ala Glu Arg Glu Lys Thr 145 Leu Arg Glu Lys Lys 150 Glu Gln Glu Leu Lys 155	1022
aac gct gca tac gaa aat gcc cgc ctg aaa gat gaa ctt cat gct aaa Asn Ala Ala Tyr Glu Asn 160 Ala Arg Leu Lys 165 Asp Glu Leu His Ala Lys 170	1070
agt ctt cag ctc aaa caa atc gaa act gat gtt gcg gta tta aaa gag Ser Leu Gln Leu Lys 175 Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu 185	1118
cgg gtg acg gaa acg aaa agc cgg ctt ttg gag gct gaa aaa aca aaa Arg Val Thr Glu Thr Lys Ser Arg Leu 195 Glu Glu Ala Glu Lys Thr Lys 200	1166
gaa gcg ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat Glu Ala Leu Phe Tyr Glu Thr 210 Ile Leu Ser Tyr Lys 215 Arg Gln Leu Asp	1214
gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt Glu Ser Asp Lys Trp Ile 225 Ala Ser His Phe 230 Ala Asp Ile Asp Ala Phe 235	1262
cag cag acg gag aag gcg ctt gaa caa aac gag gag gtt ttt gaa cgg Gln Gln Thr Glu Lys 240 Ala Leu Glu Gln Asn 245 Glu Glu Val Phe Glu Arg 250	1310
aca gaa cag atc gag gcg gtg ctt caa act gtt aca gag caa gtt gat Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp 265	1358
cag ctc caa caa caa ttg agc gcc att caa caa aat tat acg aaa atg Gln Leu Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met	1406

10295.204.ST25.txt

270

275

280

gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc 1454
 Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro
 285 290 295

ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa 1502
 Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys
 300 305 310 315

cct tta aat taaataccac ttaaggaat aatttggttt ttacaaaaaa 1551
 Pro Leu Asn

accgcttgag tagattgtct caagcagttg attgggaggc ggcgtataaa gcggccgcct 1611
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 ctgtctcagt agaaatctca ccttctaata tatattgacc gcggtatggt tttttgactt 1731
 ccgggtacat ttaaatcagg ctttgcataa aggttgtcat attagggatc tcaagtccgc 1791
 tctctttttc gatttctttt tgaagttcgg agcttttgat ggccgcatta tggcgtttta 1851
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 ttctgcgcct tgtcgttcca tctggaattc cggcaggcag tgaggagggt tgcggagaag 1971
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<210> 113

<211> 318

<212> PRT

<213> Bacillus licheniformis

<400> 113

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Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg Ser His Gln Leu Ile
 20 25 30

His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser
 35 40 45

Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu
 50 55 60

Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu
 65 70 75 80

Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu
 85 90 95

Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys
 100 105 110

His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Lys Ser
 115 120 125

10295.204.ST25.txt

Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys
 130 135 140

Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu
 145 150 155 160

Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys
 165 170 175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr
 180 185 190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr
 195 200 205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp
 210 215 220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys
 225 230 235 240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu
 245 250 255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln Gln
 260 265 270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr
 275 280 285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val
 290 295 300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn
 305 310 315

<210> 114
 <211> 2341
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1838)

<400> 114
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 agcccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg 180
 aagaagcggg agatcaaaat aaaaaagaaa cagaagcttt atttttctat aatccccgaca 240

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tcgcttctga tgactggatt aaaacgagaa aagtcgtgaa gcgcatcggc aatcatgtct	300
ttgcgatcta gaaagcagtc agggccattc gccttggctg ctttttttgt gcgattcttt	360
cttacgcatt atcatctttc acagcccaag aaaaaattta tttttgatac tttatgaaaa	420
tcaattttca attaaaaaga aaataatttt tagacttgtc tcatatgatg ggataaaccc	480
gtgagacaag gagagacctc atg aac cgt ttt gta aaa gga atc gtt ctt ctt	533
Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu	
1 5 10	
tcg cta gct gct ttt ttt gca gaa tgt ctt gaa ttc gtc atc aac atg	581
Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met	
15 20 25	
att ctt gca cgg gag ctt ggc gag cat ggc atg ggg ctc tac atg agt	629
Ile Leu Ala Arg Glu Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser	
30 35 40	
gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg	677
Val Leu Pro Ser Ile Phe Leu Val Val Ile Ala Ser Leu Glu Leu	
45 50 55	
ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac	725
Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His	
60 65 70 75	
gaa agc atg ctg aaa cat gca ttg cgg atg act gcg gtc tgc acg gtt	773
Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val	
80 85 90	
ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt	821
Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe	
95 100 105	
gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct	869
Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro	
110 115 120	
acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag	917
Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln	
125 130 135	
caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag	965
Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln	
140 145 150 155	
ctc atc ggc ttg ttt tta ttt ttt caa tgg tat tcc ttt gaa ttg gat	1013
Leu Ile Gly Leu Phe Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp	
160 165 170	
act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc	1061
Thr Ser Leu Leu Ile Ser Leu Phe Val Leu Val Ala Ser Glu Val Val	
175 180 185	
gtg ttt gtt tat ttg ttt tcg cag ttt gtt ttg gtc agg cgt gcc gct	1109
Val Phe Val Tyr Leu Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala	
190 195 200	
caa aaa ggg cag cag atc cac ttg cgg aga aac gat gtt tta aaa cgc	1157
Gln Lys Gly Gln Gln Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg	
205 210 215	
ctg ctc act gtt tcg atc ccg acg acg ggg ctg cgc gtg ttt cat gct	1205
Leu Leu Thr Val Ser Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala	
220 225 230 235	

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10295.204.ST25.txt

gtg aca aat gcc gtc gaa cct ttt ttg gtg aag ggg acg ctg ctt gcc Val Thr Asn Ala Val Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala 240 245 250	1253
gct ggc gta tca aga aca tcg gcc atc gac cag ttc ggc atg ctt tcg Ala Gly Val Ser Arg Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser 255 260 265	1301
gga gtt gcg atg aca atc ggc ttt ttt ccg gct ttt atc gcc cat tca Gly Val Ala Met Thr Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser 270 275 280	1349
ctg atg gtc gtc atg atc ccg agc att tct gaa agc tac gct tac ggg Leu Met Val Val Met Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly 285 290 295	1397
caa tac gaa aga gtg atc aaa cgg att aaa cag gcg atc ttt att acg Gln Tyr Glu Arg Val Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr 300 305 310 315	1445
ctg ttt tac ggc ata ccg tcc gtc atg gtg atg tat cac ttt gca gag Leu Phe Tyr Gly Ile Pro Ser Val Met Val Met Tyr His Phe Ala Glu 320 325 330	1493
ccg ctg acc cat tta ttt ttc gat tcg gtc aag gcg tcg ttt tac ctt Pro Leu Thr His Leu Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu 335 340 345	1541
aaa atg ttg tgg ccg tat ttt tta ttc cac ttt ttt gcg atg cct ttt Lys Met Leu Trp Pro Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe 350 355 360	1589
cag gcc tgt tta atc gga atg ggg ttg gcc aaa gat gct ttt tat cat Gln Ala Cys Leu Ile Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His 365 370 375	1637
aac gtt tgg gcc agt gtc tta tcg ttt ttg atg atg tat gtt ctc ggg Asn Val Trp Ala Ser Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly 380 385 390 395	1685
tcc atg cag act ttg cag atg acg ggg atc att ctt gcg atg aat acc Ser Met Gln Thr Leu Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr 400 405 410	1733
ggt atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu 415 420 425	1781
ctg ggc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile 430 435 440	1829
gaa agc cgc tgatggatcc tcttcatagt tttagctttt gcggggaagc Glu Ser Arg 445	1878
taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc	1938
ctgctgtttt ttaccgggtt attcgtattt cagccgcagg catctgcaaa acaagcttcg	1998
ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc	2058
cagaagacga tcgttcattt ttggacgacc tgggtgccgc catgccgtga agagcttccg	2118
cgattccaat cctactatga aagcaagcaa tccggcgtca agctcgtgac cgtaattta	2178
ctgaatgccg aaaagaacga acagaaggta aaacagttaa ttaaagcaaa caagctgaca	2238

10295.204.ST25.txt

ttttccgatcg tttttgacaa aaagggtgag atgatgaaag catataaagt catgacaatt 2298
 cctacgactt ttttcttttaa tgaaaaagga gagctggaga aaa 2341

<210> 115
 <211> 446
 <212> PRT
 <213> Bacillus licheniformis

<400> 115

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Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met Ile Leu Ala Arg Glu
 20 25 30

Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile
 35 40 45

Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser
 50 55 60

Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys
 65 70 75 80

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala
 85 90 95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro
 100 105 110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr
 115 120 125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile
 130 135 140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe
 145 150 155 160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile
 165 170 175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu
 180 185 190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln
 195 200 205

Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser
 210 215 220

10295.204.ST25.txt

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val
225 230 235 240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg
245 250 255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr
260 265 270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met
275 280 285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val
290 295 300

Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile
305 310 315 320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu
325 330 335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro
340 345 350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile
355 360 365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser
370 375 380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu
385 390 395 400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu
405 410 415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu
420 425 430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg
435 440 445

<210> 116
<211> 1417
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (420)..(914)

<400> 116

10295.204.ST25.txt

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 gacagagact tcgaacatgc cggcaagctc ctttgcctgc acttggcgtt tattaatcaa 180
 taaaatcaca atggccaaaa gccgggtcaat tttcactgca gatccctcac attcatcttg 240
 tgcagcctct ttttttctgc tatttttctt ccatagcgca caccattctg ggatatcatg 300
 acaaaaaaga ggatctcatc acccatttat ctagaaaacc acttttcagg ttacgatttg 360
 tacagtttgg acatatactc cttaaaaaag gaggttttaa aaacatcata ttttatttt 419
 ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cgg 467
 Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
 1 5 10 15
 tgc gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cgg atc 515
 Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
 20 25 30
 atc ctt ttt tgc gga att ttc gtt ttt ctg ctg acg atg agc gca ctt 563
 Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
 35 40 45
 cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc 611
 His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
 50 55 60
 atc ttg acc gtc tat gcg ctg aag cat gtg tgc atc gaa aat cgg ggc 659
 Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
 65 70 75 80
 gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc 707
 Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
 85 90 95
 ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag 755
 Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
 100 105 110
 ctg cag act gcg gtt tca gac ggg ggt tgc gca gct tac ggc gcc ctt 803
 Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
 115 120 125
 ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt 851
 Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
 130 135 140
 tat tat gtc ggt ttc tct ttt ttt gtt tta aaa aaa ggc aga acc gaa 899
 Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
 145 150 155 160
 gaa aag cgc tca gct taaaaaggca aactcgggaa attgagtttg ctttttaaac 954
 Glu Lys Arg Ser Ala
 165
 tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctgggtctt 1014
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 aaaacctgag ctggtgagaa acgggtgact gcaggagact cagcttctct gctatttcat 1134
 taaccgaatg ctgccttgt gagagcaggt gaagaatttt gattctcggt gggtcagaga 1194
 gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccgacact 1254

10295.204.ST25.txt

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 tacctccata tcatatacca aaacataccg gttgaaaagt tttaacggat caagtcgaaa 1374
 acagcgttcc ttgaagcgct tctacatatc ttgcagcaga cct 1417

<210> 117
 <211> 165
 <212> PRT
 <213> Bacillus licheniformis

<400> 117

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 20 25 30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
 35 40 45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
 50 55 60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
 65 70 75 80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
 85 90 95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
 100 105 110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
 115 120 125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
 130 135 140

Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
 145 150 155 160

Glu Lys Arg Ser Ala
 165

<210> 118
 <211> 2353
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1850)

10295.204.ST25.txt

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 gggcggattc tcgaacaacg acattaatct gttggcccaa gcggtttacg gtgaagcgcg 180
 cggagaaccg tatgacggcc aggttgccgt tgcagctggt atattaaaca ggctcgatag 240
 ccctacgttc ccgaatacgg tggcggggcg tatctttgaa ccgcttgcat ttacagctgt 300
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 ataaaagcga ggtgctataa atg atc aga gga att tta atc gcc ctt tta ggt 533
 Met Ile Arg Gly Ile Leu Ile Ala Leu Gly 10
 gtc gcc atc gtc gga aca agc tat tgg ggc tat aaa gaa cat cag gag 581
 Val Ala Ile Val Gly Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu 25
 aaa gac gcc gtt ttg ctt cat gcc gaa aac aac tat caa agg gca ttt 629
 Lys Asp Ala Val Leu Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe 40
 cac gac tta act tat cag gtg gat cag ctg cat gat aaa atc ggg agc 677
 His Asp Leu Thr Tyr Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser 55
 acg ctt gcg atg aac agc aaa aaa acg ctg tct ccc gct ttg gcg gaa 725
 Thr Leu Ala Met Asn Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu 70
 gtc tgg aaa acg act tct gaa gcg cat aac aat gtc agc cag ctg ccg 773
 Val Trp Lys Thr Thr Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro 85
 ctg acc tta atg ccg ttt aac aag acc gaa gag ttt ttg gca aag gtc 821
 Leu Thr Leu Met Pro Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val 100
 gga gat ttc agc tac aaa gca gcc gtg cgc gat ctt gac aaa gag ccg 869
 Gly Asp Phe Ser Tyr Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro 110
 ctc aat aaa aaa gag tac gct tct tta aat cag cta tat gaa aat tca 917
 Leu Asn Lys Lys Glu Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser 130
 aag gat ata caa aat gaa ctg cgt aat gtc cag cat ttg att att gac 965
 Lys Asp Ile Gln Asn Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp 145
 aaa aat ttg aga tgg atg gat gta gaa ctt gcg ctc gcg tcc ggc caa 1013
 Lys Asn Leu Arg Trp Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln 160
 aaa caa agc gac aat aag att att aat ggc ttt aaa acc gtt gaa aaa 1061
 Lys Gln Ser Asp Asn Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys 175
 agc gca agt gca ttt tgc gat acg gat tta ggc gcg aca gag atg acg 1109
 Ser Ala Ser Ala Phe Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr 190

10295.204.ST25.txt

aac acg aaa aaa gag cag caa ggg tac gac cat tta caa ggc aaa aga Asn Thr Lys Lys Glu Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg 205 210 215	1157
ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp 220 225 230 235	1205
aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg 240 245 250	1253
gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile 255 260 265	1301
tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa Tyr Met Asp Ile Thr Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln 270 275 280	1349
aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn 285 290 295	1397
aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu 300 305 310 315	1445
aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe 320 325 330	1493
gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc Val Pro Val Gln Asp Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile 335 340 345	1541
aag gtc gcg ctt gac gac ggc gag att acc ggg ttt aat gca aag gat Lys Val Ala Leu Asp Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp 350 355 360	1589
ttc tta atc tcc cat aaa aaa aga gac ttg ccg aag ccc aaa cta acg Phe Leu Ile Ser His Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr 365 370 375	1637
cct gaa aaa gcg aaa gca agc ctg aat ccc aac gta aaa gtt cag gag Pro Glu Lys Ala Lys Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu 380 385 390 395	1685
acg cgc ctt gct tta gtc acg aac gag ctt tcg caa gaa gtg ctc tgc Thr Arg Leu Ala Leu Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys 400 405 410	1733
tac gaa att ctc ggc acg att gaa aac gat aca ttc cgc atg ttc atc Tyr Glu Ile Leu Gly Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile 415 420 425	1781
aat gcc aat gac ggc acg gaa gag aag gtt cag aaa atg aaa agc gca Asn Ala Asn Asp Gly Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala 430 435 440	1829
gaa ccg ata tac aac gac ttg taaaaacgat agatcaaagg gaaaaggcga Glu Pro Ile Tyr Asn Asp Leu 445 450	1880
taacatgcct tttccttttt agcattcggga ataattcgcc ctaaaccattt ccatactgaa	1940
catatggggcg gaacgtccgc cggtaaattg aaaatgcccc gggccataaa ttttccgggc	2000

10295.204.ST25.txt

agcggaggaa taatatgaaa acaatcgaac ggttattatt taagatactc gtcgtacaga 2060
 cggtcatttt aatcagcgtg cagcttcttt ttcatctctc caaggctgag ccttatctgt 2120
 caaaggctcgt gcagtatgaa ggcgtgaaca acatgaaaat cggcgaatgg atcgagacat 2180
 ttaagccgta attcacgcta aaatctcccc tttttcgctt aatacatgat acaatcctat 2240
 aaggagtacc agatagcaag gagaggaatt atggaaaaga aattatgcat tgcaatagac 2300
 ggccctgcgg cagccggaaa aagcaccgtg gcgaaaatcg tggccagaaa aaa 2353

<210> 119
 <211> 450
 <212> PRT
 <213> Bacillus licheniformis

<400> 119

Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly Val Ala Ile Val Gly
 1 5 10 15

Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu Lys Asp Ala Val Leu
 20 25 30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr
 35 40 45

Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn
 50 55 60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr
 65 70 75 80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro
 85 90 95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr
 100 105 110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu
 115 120 125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn
 130 135 140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp
 145 150 155 160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn
 165 170 175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe
 180 185 190

10295.204.ST25.txt

Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu
 195 200 205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu
 210 215 220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile
 225 230 235 240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile
 245 250 255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr
 260 265 270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys
 275 280 285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe
 290 295 300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser
 305 310 315 320

Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp
 325 330 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp
 340 345 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His
 355 360 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys
 370 375 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu
 385 390 395 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly
 405 410 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly
 420 425 430

Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala Glu Pro Ile Tyr Asn
 435 440 445

Asp Leu
 450

10295.204.ST25.txt

<210> 120
 <211> 1355
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (249)..(1355)

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 tatattgaaa accacagagg gcttttgctt ttcagcgata cggaagtaag gctgatgctc 120
 aaacagggggc agtgcacat tcaaggcaaa gactttgtca tcaaaacgat ttgacctgag 180
 gaaattctgc ttgaaggcac gattgagctt gtccgctata tcgattcata agtcgggggg 240
 aaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga aag atc cag 290
 Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln
 1 5 10
 ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat gaa tgc acc 338
 Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr
 15 20 25 30
 agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa gac gcc gtc 386
 Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val
 35 40 45
 ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg aag gtc atc 434
 Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile
 50 55 60
 aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa ggg ttt cct 482
 Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro
 65 70 75
 ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act ttt gga gtt 530
 Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val
 80 85 90
 gct gca ttt ttt atc atc atg ttc cta ttg tcc aac atg ctt tgg aaa 578
 Ala Ala Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys
 95 100 105 110
 att gat att aca gga gcc aat cca gag aca gaa cat caa atc aga cag 626
 Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln
 115 120 125
 caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag ttt tca atg 674
 Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met
 130 135 140
 ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg gtc gaa aac 722
 Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn
 145 150 155
 atc act tgg gtg ggc att gag tta aac ggt acc gcc ctt cac atg aaa 770
 Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys
 160 165 170
 gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc ggt ccg agg 818
 Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg
 175 180 185 190

10295.204.ST25.txt

cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa atg ttc gtg gaa 866
 His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu
 195 200 205
 aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa 914
 Lys Gly Glu Pro 210 Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln
 215 220
 atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc 962
 Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val
 225 230 235
 gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta 1010
 Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val
 240 245 250
 acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt aaa gta agg 1058
 Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg
 255 260 265 270
 aca agt cac aag cta tcc ctc gga tca tta acc atg ccg atc tgg ggc 1106
 Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly
 275 280 285
 ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa 1154
 Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu
 290 295 300
 aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa 1202
 Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu
 305 310 315
 aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa 1250
 Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys
 320 325 330
 aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag 1298
 Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln
 335 340 345 350
 gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca 1346
 Asp Lys Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala
 355 360 365
 cac cac gag 1355
 His His Glu

<210> 121

<211> 369

<212> PRT

<213> Bacillus licheniformis

<400> 121

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys
 1 5 10 15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg
 20 25 30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val Phe Leu
 35 40 45

10295.204.ST25.txt

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
 50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
 65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
 85 90 95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
 100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu
 115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
 130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
 145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
 165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
 180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly
 195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
 210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
 225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
 245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
 260 265 270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser
 275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His
 290 295 300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
 305 310 315 320

10295.204.ST25.txt

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
 325 330 335

Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln Asp Lys
 340 345 350

Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala His His
 355 360 365

Glu

<210> 122
 <211> 2120
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1625)

<400> 122
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 ttaccaagat ctcggcttaa aggcgacaaa gctgacaaag gaaaaagcaa tcgacgaagg 120
 cccgggctac acgagcattt ccttagaaaa gctgcctgat ttcgctggag attatatatt 180
 tataggacct tgggaatcaa gcggagacga cagcgccgtg cttatacat ccatttgga 240
 gaaccttggg gcggtcaaaa accaacaatgt ctataaaatc gaccctgtcg gcttctattt 300
 ttccgatccg atttcattag agggccagct cgaatttatt acagaaaact taacaaaata 360
 gaagaacttc cgccttgtca ggcggaagtt ttttttgcgc gcgaaaccgg ggtgaaccct 420
 cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata 480
 tgctattgtg ggagggatca ttg atg gca ttc atc aac atc aaa ccg gag tta 533
 Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu
 1 5 10
 aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg 581
 Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro
 15 20 25
 ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt 629
 Leu Leu Ile Ser Ala Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe
 30 35 40
 ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca 677
 Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr
 45 50 55
 tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa 725
 Tyr Glu Gln Leu Gln Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu
 60 65 70 75
 cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag 773
 Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys
 80 85 90
 gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc 821
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Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile
 95 100 105
 869
 atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga
 Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly
 110 115 120
 917
 gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc
 Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
 125 130 135
 965
 aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac
 Asn Glu Trp Ile Thr Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr
 140 145 150 155
 1013
 tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc
 Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu
 160 165 170
 1061
 gat att ttt tca tca aca aag ctt tcc gtc gtg ccg atc gtt aat ccc
 Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro
 175 180 185
 1109
 gac ggt gtt gac ctt gta ctt aac ggc ccc ggt cat ctt ggg atc gcg
 Asp Gly Val Asp Leu Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala
 190 195 200
 1157
 aga gaa gcg ctg gat gag atg aac gag cat cag ccg gat ttc cgg gaa
 Arg Glu Ala Leu Asp Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu
 205 210 215
 1205
 tgg aaa gcc aat ata aac gga gtg gat tta aat aat cag ttt ccg tct
 Trp Lys Ala Asn Ile Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser
 220 225 230 235
 1253
 ttc tgg gag atc gaa aaa caa aga aaa ccg cct aaa tcc cct tcc tac
 Phe Trp Glu Ile Glu Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr
 240 245 250
 1301
 aga gac tac ccc gga gat gaa ccg ctg aca gaa ccg gaa gcg gca gcg
 Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala
 255 260 265
 1349
 atg agg gat tta atc gca aac gag ccg cct gac cgg ctt gtg gcg ctt
 Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu
 270 275 280
 1397
 cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct
 His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro
 285 290 295
 1445
 cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat
 Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr
 300 305 310 315
 1493
 aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg ttt
 Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe
 320 325 330
 1541
 att cat tat tac gga aga gaa gga tat act gtt gaa ctt ggc aaa gga
 Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly
 335 340 345
 1589
 aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc
 Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser
 350 355 360
 1635
 aga gga ata ctt tgg gca tcc tgt ttt ttt gaa agc tgaaactttt

10295.204.ST25.txt

Arg Gly Ile Leu Trp Ala Ser Cys Phe Phe Glu Ser
 365 370 375

cacgggtgaaa atcgtaaatt agacagccaa acatttatgg agggagaatg gccggtttga 1695
 gagtttcatt attgattatt gccgctctga tggccgtggc tgcggctggt tgcacgccgc 1755
 agcatcaaga aggatcaaaa agcgttcac atgaggagcc ggaagggaaa agagaaagcg 1815
 gtgcagcagt aaaagataaa aaagtgatag cgctgaagga ccggcacttt gatgagacgg 1875
 caggatggct tgataatgaa accgttatat acaccgcaac cgatccggtc ggaggaagtg 1935
 aaatcaaadc atatgatata tttaaagggc cgggcaaaac gatctacaag acagatgaca 1995
 ggctgatagc gtcggaagtc aacagtgaaa aaggcatgat tcttatccaa accgccggaa 2055
 acggctctga aatgaagtta actttgctta atttacaggg gaaacagctg tttgcaaaaa 2115
 aattt 2120

<210> 123
 <211> 375
 <212> PRT
 <213> Bacillus licheniformis

<400> 123

Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu Lys Gln Asn Met Glu
 1 5 10 15

Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro Leu Leu Ile Ser Ala
 20 25 30

Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe
 35 40 45

His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln
 50 55 60

Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys
 65 70 75 80

Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu
 85 90 95

Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser
 100 105 110

Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly
 115 120 125

Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr
 130 135 140

Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys
 145 150 155 160

10295.204.ST25.txt

Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser
 165 170 175
 Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu
 180 185 190
 Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp
 195 200 205
 Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile
 210 215 220
 Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu
 225 230 235 240
 Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly
 245 250 255
 Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile
 260 265 270
 Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu
 275 280 285
 Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp
 290 295 300
 Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr
 305 310 315 320
 Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly
 325 330 335
 Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro
 340 345 350
 Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser Arg Gly Ile Leu Trp
 355 360 365
 Ala Ser Cys Phe Phe Glu Ser
 370 375

<210> 124
 <211> 1597
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (342)..(1094)

<400> 124

10295.204.S125.txt																		
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aaagcgatgg	tcattctcaa	actgtaacca	attattttct	tgatagtgtg	gctgcgacta													120
ttatgcgctg	attgttttac	gtgcttgctt	tttataccat	tggttcattt	gaccggaatc													180
gtgttttgat	tgcaggaatt	tttgtttact	tttgtgaaaa	aacagcagaa	gaaaaacagc													240
ggaaaactcg	cgtcttaggg	cggattttcca	aaaaaatgtc	gtaaattcga	tgcattcaatt													300
tgatgaaatc	gcccggccat	gcggtataat	agattttgtg	a	atg	aaa	gat	tca	atg									356
					Met	Lys	Asp	Ser	Met									
					1				5									
ttg	aaa	gag	agt	ggt	tac	atc	atg	ggc	cgt	aaa	tgg	aac	aat	ata	aaa			404
Leu	Lys	Glu	Ser	Gly	Tyr	Ile	Met	Gly	Arg	Lys	Trp	Asn	Asn	Ile	Lys			
				10					15					20				
gag	aag	aaa	gcg	tcc	aag	gat	gcg	aat	acg	agc	cga	atc	tac	gcg	aag			452
Glu	Lys	Lys	Ala	Ser	Lys	Asp	Ala	Asn	Thr	Ser	Arg	Ile	Tyr	Ala	Lys			
			25					30					35					
ttc	ggc	cg	gaa	atc	tat	gtg	gcg	gca	aag	cag	gga	gag	ccc	gat	ccc			500
Phe	Gly	Arg	Glu	Ile	Tyr	Val	Ala	Ala	Lys	Gln	Gly	Glu	Pro	Asp	Pro			
		40					45					50						
gaa	ctg	aac	cag	aac	ctg	aaa	ttc	gtg	ctt	gag	cg	gcc	aaa	aca	tac			548
Glu	Leu	Asn	Gln	Asn	Leu	Lys	Phe	Val	Leu	Glu	Arg	Ala	Lys	Thr	Tyr			
	55					60					65							
aat	gtc	ccg	aaa	gcg	att	gag	cg	gcg	atc	gaa	aaa	gcg	aag	ggc				596
Asn	Val	Pro	Lys	Ala	Ile	Glu	Arg	Ala	Ile	Glu	Lys	Ala	Lys	Gly				
70					75				80					85				
ggc	tct	gag	gaa	aat	tac	gac	gag	ctg	cg	tat	gaa	ggc	ttc	gg	ccg			644
Gly	Ser	Glu	Glu	Asn	Tyr	Asp	Glu	Leu	Arg	Tyr	Glu	Gly	Phe	Gly	Pro			
				90					95					100				
aac	gga	gcg	atg	gtg	atc	ggt	gac	gcg	ttg	aca	aac	aac	gtc	aac	cg			692
Asn	Gly	Ala	Met	Val	Ile	Val	Asp	Ala	Leu	Thr	Asn	Asn	Val	Asn	Arg			
			105					110					115					
acg	gct	gcc	gat	gtg	cg	tcc	aca	ttt	ggc	aaa	aac	ggc	gga	aac	atg			740
Thr	Ala	Ala	Asp	Val	Arg	Ser	Thr	Phe	Gly	Lys	Asn	Gly	Gly	Asn	Met			
		120					125					130						
gga	gtg	agc	gga	tct	gtc	gct	tac	atg	ttt	gat	ccg	acg	gcc	gtc	atc			788
Gly	Val	Ser	Gly	Ser	Val	Ala	Tyr	Met	Phe	Asp	Pro	Thr	Ala	Val	Ile			
	135					140					145							

10295.204.ST25.txt
225

215 220 - 1076
 ctg att gac gcg ctg gaa gat ctg gaa gac gtt cag caa gtt tac cat
 Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val Gln Gln Val Tyr His
 230 235 240 245
 1124
 aat gtc gat tta ggg gcg taaaaagagg ccctgaaaaa atcgggaaag
 Asn Val Asp Leu Gly Ala
 250
 1184
 aaaagataga tgaacaggag gacgacctgt tttgtctatc tttttttatt gtaaagttaa
 1244
 cttgacattt ttttttttg ttaagtatac tttacgtata gtgaacttta cattcccaat
 1304
 ggaggaaaga tgaacacgtt aataaaggaa aagcgacatt cgctgaacat gacacaagaa
 1364
 gaactggcta aaaggcttaa tgtgtcgagg caaacggtga tttcccttga aaagggaaaa
 1424
 tataaacctt cactcgttct ggcgcataaa ctggctcaaa tttttgaatg tctgattgaa
 1484
 gatttattta tttttgaggg ggatgaaaat attgactgaa acgatgacaa acatactgat
 1544
 cgcttttagcg ggcttagaat aggcgtgctc gggatcgcaa ttgtttacaa agtaaacaga
 1597
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<210> 125
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 <213> Bacillus licheniformis

<400> 125

Met Lys Asp Ser Met Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys
 1 5 10 15

Trp Asn Asn Ile Lys Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser
 20 25 30

Arg Ile Tyr Ala Lys Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln
 35 40 45

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu
 50 55 60

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile
 65 70 75 80

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr
 85 90 95

Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr
 100 105 110

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys
 115 120 125

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp
 130 135 140

10295.204.ST25.txt

Pro Thr Ala Val Ile Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu
145 150 155 160

Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu
165 170 175

Asp Asp Ala Val Ile Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val
180 185 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu
195 200 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg
210 215 220

Ala Gln Phe Glu Lys Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val
225 230 235 240

Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala
245 250

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<213> Bacillus licheniformis

<220>
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<222> (3)..(1385)

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1 5 10 15

att gct ttc tcc att cta tat ttg tcc gcc ccg ttt ttt gca gag atg 95
Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met
20 25 30

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg 143
Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val
35 40 45

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg 191
Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu
50 55 60

gcg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca 239
Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr
65 70 75

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta 287
Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu
80 85 90 95

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc 335
Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val
100 105 110

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10295.204.ST25.txt

gct gtc ggc tat gcg act ttt gcg gct ttg atc gga gcg ttc gcc gga 383
Ala Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly
115 120 125

ctg ttc act ctt tac ttt tcc tgg cag aaa aga aaa ggg gcg ctc ctg 431
Leu Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu
130 135 140

gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa 479
Ala Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln
145 150 155

atg ttt aaa gag ctg ttc agc tat gcc gcc cct tat gtc ttt gtc ggg 527
Met Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly
160 165 170 175

ctg gcg ata ccg ctt tac cag tac att gat acg aat acg ttt aat aaa 575
Leu Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys
180 185 190

gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg 623
Ala Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala
195 200 205

atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc 671
Ile Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu
210 215 220

gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt 719
Ala Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe
225 230 235

acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg 767
Thr Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met
240 245 250 255

cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt 815
Gln Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu
260 265 270

ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc 863
Leu Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu
275 280 285

cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg 911
Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu
290 295 300

tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac 959
Leu Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn
305 310 315

aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa 1007
Lys Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys
320 325 330 335

atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg 1055
Ile Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser
340 345 350

att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt 1103
Ile Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe
355 360 365

atc atg att aaa cgc cat gcc ggc tat tcg tat cgc aaa ctg ttt aaa 1151
Ile Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys
370 375 380

10295.204.ST25.txt

cgg ttt ttg ctg atg ctg atc ctg acg gcg gtc atg ggc atc att ttg 1199
 Arg Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu
 385 390 395
 ctg ctt gtc cag gcg ctt cta agt att ttt att tca tac gaa ggc ggg 1247
 Leu Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly
 400 405 410 415
 cag atc agg tct gct gtc gtc att ttc atc aca acc gca gtg ggc ggg 1295
 Gln Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly
 420 425 430
 tca gtt tat ctg tac ttg gct tac cgt gtg aaa ctg ctc gaa aaa atc 1343
 Ser Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile
 435 440 445
 ttc ggt cag cga ttg aat cgc ttt ttc aaa aga aag gcc tcc 1385
 Phe Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
 450 455 460
 taaaaagggc ttttcttttt atgtaaaaaa aggggtgtct tcatgagatt ggataaactg 1445
 ttgtcaaaaca gcggctatgg ttcgagaaaa gaagtcaaaa aaatgctgaa aaacggcgcg 1505
 gtgcgcgtca atgatcaatt agtcaaagac gccaaaaagc acgttgaccc ggaatcagac 1565
 gacatcacgg tatacggggc acccgatcatg taccgggaat ttatttactt aatgatgaac 1625
 aagccgcaag gagtgctgtc agcaacagaa gacagccggc aggaaacggt tgtcgatttg 1685
 ctcgaccccg agctgctgag gtttgagccg tttcctgtcg gaaggcttga caaggatact 1745
 gagggactgc tgcttctgac gaatgacgga cagttggcac accagctttt atctccgaaa 1805
 aaacacgtac ctaaaacgta tgaagtccat gtcaataagc cgattgatca agcggcactt 1865
 gatcagcttg aaaaaggggt cga 1888

<210> 127
 <211> 461
 <212> PRT
 <213> Bacillus licheniformis

<400> 127

Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile Ile
1 5 10 15

Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala
20 25 30

Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr
35 40 45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala
50 55 60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala
65 70 75 80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr
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10295.204.ST25.txt
90

85

95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala
100 105 110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu
115 120 125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala
130 135 140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met
145 150 155 160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu
165 170 175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala
180 185 190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile
195 200 205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala
210 215 220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr
225 230 235 240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln
245 250 255

Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu Leu
260 265 270

Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu Pro
275 280 285

Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu Leu
290 295 300

Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn Lys
305 310 315 320

Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys Ile
325 330 335

Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser Ile
340 345 350

Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe Ile

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca 677
Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala
Page 185

10295.204.ST25.txt

55

45 50 55
 acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca 725
 Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr
 60 65 70 75
 gag cgg gaa ggc caa tat gaa ctc ata gcc gga gag cgg cgc tgg cgg 773
 Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg
 80 85 90
 gcg gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat 821
 Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp
 95 100 105
 ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag 869
 Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln
 110 115 120
 agg gaa gaa tta tct tcg att gaa gag gcg cat gct tat gca agg ctt 917
 Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu
 125 130 135
 tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga 965
 Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly
 140 145 150 155
 aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg 1013
 Lys Gly Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro
 160 165 170
 gaa gag gtg cag gaa gcg atc ttg aaa aaa gaa att tca gag cgc cac 1061
 Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His
 175 180 185
 gca aga gcg ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg 1109
 Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu
 190 195 200
 ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac 1157
 Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp
 205 210 215
 cgt gtc gtc aaa atg ctt gag cag gat aaa cgc aag cct aaa cca aag 1205
 Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys
 220 225 230 235
 aga aaa gcg tac agc agg gac gcg aga atc gcg atg aat acg att cgc 1253
 Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg
 240 245 250
 cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa 1301
 Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu
 255 260 265
 gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa 1349
 Glu Glu Glu Phe Glu Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
 270 275 280
 taaaagctcc ctatagagct tttatttttt taggcaaaat atctatgggg gagcgtctat 1409
 ggaatattat cgacaatatc attcattgct tttttcgatt gcttaccgta tgctcgggtc 1469
 ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat 1529
 cgggtcaaatt gaccatattc aagcatatatt aacgaaatca atcaciaaacc gctgcataaa 1589
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10295.204.ST25.txt

gcaggtggcg ctttcagctc aaatcccggc tgagtacgtt gaagagaaag aaaaggtatc 1709
 ctatgctttt ctggtagtta tgagccgatt aaatcctgta gaaagagccg ttttgatggt 1769
 tagagaagta tttggatatc attacaagga aatttcgtcc attatcgga agtcggaagc 1829
 gaactgtcgt caaatccaca gcc 1852

<210> 129
 <211> 283
 <212> PRT
 <213> Bacillus licheniformis

<400> 129

Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu Gly Asp Lys Glu Glu
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 Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys Glu Glu Ile Gln Glu
 20 25 30
 Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile
 35 40 45
 Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His
 50 55 60
 Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln
 65 70 75 80
 Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu
 85 90 95
 Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu
 100 105 110
 Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser
 115 120 125
 Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp
 130 135 140
 Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr
 145 150 155 160
 Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu
 165 170 175
 Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile
 180 185 190
 Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile
 195 200 205

10295.204.ST25.txt

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met
 210 215 220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser
 225 230 235 240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met
 245 250 255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Glu Phe Glu
 260 265 270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
 275 280

<210> 130
 <211> 1495
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(995)

<400> 130
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 tcgtccatga gcctgatgcc gctttaacgg caaatcaata ccccgatcaat ctgcaaatat 120
 ccggacacac ccacgcgcgg acaaattcag attcctgtat tcggtccttt gattacgcct 180
 ccgtacgtag acgtttatac gcaaggaatg tatgcaacag ccggaatgaa aatttatgtc 240
 atttgaggaa tcggcacgag caggctgccg ctccgctttc tgtcaaagcc tgaaatcacc 300
 gtgttcacgc ttgaatccat ttaattcttg ccggtccttt ggctcaaaac aaaaggcatc 360
 tgcatacatt aagtaaaaac attcccgtc catttcatcc aatcccatca aaaaaacgga 420
 acttcctcag cctcttccgt ctatatatta gcagcggaaa aggtctctctt ttcgtttttg 480
 aaaaggagat gtgctgatta ttg ctg atg tac caa gtc aaa ccc gga gga acc 533
 Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr
 1 5 10

ctt gaa agc atc gcc gcc gat ttc aga acg acc cgg cag gcg ttg ctg 581
 Leu Glu Ser Ile Ala Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu
 15 20 25

cag gcg aat cct ggc tta aac ggc ggc caa gtg tcc gcg ggc cag tcg 629
 Gln Ala Asn Pro Gly Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser
 30 35 40

att atc att ccc ggc atc aga aat ccg gac aca att cca tac cgg att 677
 Ile Ile Ile Pro Gly Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile
 45 50 55

gcc gtg tct ctc aac gga aga acg ctc aga ttg tat gag cga gac aga 725
 Ala Val Ser Leu Asn Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg
 60 65 70 75

ctt gta aaa aca tat ccg att gcc gtc gga aaa atc ctc aca cag acg 773
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10295.204.ST25.txt

Leu Val Lys Thr Tyr Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr
 80 85 90

ccg aga ggc gaa ttt gtc atc gtc aac cgg cag cca aat ccg ggc ggc 821
 Pro Arg Gly Glu Phe Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly
 95 100 105

ccg ttc ggc gcc tac tgg ctg agc ctg tca aaa cag cac tac ggc atc 869
 Pro Phe Gly Ala Tyr Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile
 110 115 120

cat gga acg aat aac cct tcg tca att ggc aaa gct gtt tca agg gga 917
 His Gly Thr Asn Asn Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly
 125 130 135

tgt atc cgc atg cac aat cgg gat gtt ctg gaa ctt gct tct atc gta 965
 Cys Ile Arg Met His Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val
 140 145 150 155

ccc aac gga acc cga gtg tcc att aca cct tagacgagta catttccaga 1015
 Pro Asn Gly Thr Arg Val Ser Ile Thr Pro
 160 165

caaatgcaat ttgaacaata caacatcttg tattaagata taatgggacc tttagggttaa 1075

ggagcgtata tatggatctt tttaaaaatc gtaatttcgt cggacttttt ttcgcagctt 1135

tcgcttctca aatgggaacg acagtcggaa atatggcttt cgcctttttc ttgctcgacc 1195

ggttcagcag ccagccggcc tatacgacaa tcgccgagct gatgtattcc ttgccgacgg 1255

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aaaactgtga ttggatcaga ggcgggactg actgtcgttc ttttctttgt attgtatctt 1375

caaattatac cgcttggtt tttagtccta tttatcagaa gcgcgggttac aaaatttttc 1435

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<211> 165

<212> PRT

<213> Bacillus licheniformis

<400> 131

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 1 5 10 15

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 20 25 30

Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser Ile Ile Ile Pro Gly
 35 40 45

Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile Ala Val Ser Leu Asn
 50 55 60

Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg Leu Val Lys Thr Tyr
 65 70 75 80

Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr Pro Arg Gly Glu Phe
 Page 189

10295.204.ST25.txt

85

90

95

Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly Pro Phe Gly Ala Tyr
 100 105 110

Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile His Gly Thr Asn Asn
 115 120 125

Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly Cys Ile Arg Met His
 130 135 140

Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val Pro Asn Gly Thr Arg
 145 150 155 160

Val Ser Ile Thr Pro
 165

<210> 132
 <211> 1897
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1397)

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 tatttgtccc tcagcctaac gtagattccg cggtcatcag gctgacgctg aggaaagagc 120
 cggctgtggc cgttcaagat gctgcctttt tctttcaagt cgtaaaagca agctttgcac 180
 agcgtcgaaa aacgctttttc aacaacctcg tcaacaatct gccgaatggc aaagagaata 240
 aatcaaaaat tgaaagagcg cttcaggatt cacatatcga cggaaaacga cgcgagagat 300
 cgcttagcat tgaagagttc gccgtcttat ctgaccgctt gagagaagtc cttctttaat 360
 ggagggcttt ttttattgat gccgggcttt aagcctgata aggcttgta tccgttcacc 420
 acttgaaggg caggcacata ggctaaagaa gcacctttac tttttcgttg cttgatgttc 480
 atcaggatgg ggcttagtct atg tgt gga gtg aaa agc atg caa ttt aaa ata 533
 Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile
 1 5 10

ggc gat atg gtc gtc aga aaa tct tat cga aga gat att tta ttt cga 581
 Gly Asp Met Val Val Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg
 15 20 25

att ata aga att gat caa tcg gca aat gga gaa cct gta gcc gtt ttg 629
 Ile Ile Arg Ile Asp Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu
 30 35 40

cac gga gat gag gtc aga tta atc gct gac gcg cat ttg ggg gat ctt 677
 His Gly Asp Glu Val Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu
 45 50 55

gag att gtc cgc gag gct gag tgg cag atg aga aag cgg gaa gaa gaa 725
 Glu Ile Val Arg Glu Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu
 Page 190

10295..204.ST25.txt

60	65	70	75	
acg aga atg aag gaa tcc ctc gat ctt ctc cgc cag gat tac aaa ctc				773
Thr Arg Met Lys Glu Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu				
	80	85	90	
ctt cac gat aaa cat gag tac cgc gcc aca aac caa tat aac aat caa				821
Leu His Asp Lys His Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln		100	105	
	95			
cag cag tac ttt cat atg ccc gga aga gtc ctt cat tta gac ggg gat				869
Gln Gln Tyr Phe His Met Pro Gly Arg Val Leu His Leu Asp Gly Asp		115	120	
	110			
tcg gct tat ttg aaa aag tgt ctg gcg ctc tac gaa aag atc ggg gtt				917
Ser Ala Tyr Leu Lys Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val			135	
	125	130		
cct gta tac ggc att cat tgc tat gaa aag aaa atg tca tca gtc atc				965
Pro Val Tyr Gly Ile His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile			150	155
	140	145		
gag gaa ctg atc gat gaa tac cgc ccg gat ctt ctc gtc att acc gga				1013
Glu Glu Leu Ile Asp Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly			165	170
	160			
cac gat gcc tat tct aag cag aag ggc gat att aac aat ctg gat gcc				1061
His Asp Ala Tyr Ser Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala			180	185
	175			
tac agg cat tca aaa gat ttt atc gaa acc gtt caa aaa gcg aga aga				1109
Tyr Arg His Ser Lys Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg			195	200
	190			
aaa att ccc cat ctt gat cag ctc gtc att ttt gcc ggc gca tgc cag				1157
Lys Ile Pro His Leu Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln			210	215
	205			
tcc cat ttt gaa tca ctg atc aga gcc ggt gca aat ttc gca agc tct				1205
Ser His Phe Glu Ser Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser			230	235
	220	225		
ccg tcc aga gtc aac atc cat gcg ctt gat ccg gtc tat ata gtc gca				1253
Pro Ser Arg Val Asn Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala			245	250
	240			
aaa atc agc ttc act ccg ttt atg gac cgc att aac gtc tgg gaa gtg				1301
Lys Ile Ser Phe Thr Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val			260	265
	255			
ctc aga aat acc ttg acg aga gaa aag ggg ctc gga ggt att gag acg				1349
Leu Arg Asn Thr Leu Thr Arg Glu Lys Gly Leu Gly Ile Glu Thr			275	280
	270	275		
cgg ggc gta ttg cgt att gga atg cca tat aaa aca aaa gca aac gat				1397
Arg Gly Val Leu Arg Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp			290	295
	285			
taaacgagcc cgccggatgg cgggtttttg ctatgcacac gaaatgtttt tacctttttt				1457
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tgtcacaaat atttttattga cagaggctta tgaacgttga tataattttaa atttttattg				1577
acaaaaatgg gcttctggtg tatactgaat atagtgaggt ggatgcaatg gcgaaaacgt				1637
tgtccgatat taaaagatcg cttgatggac atttgggaaa aaggctgacg ttaaaaagcaa				1697

10295.204.ST25.txt

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 cggatattct tactgagacg gttgaattga ggttttccga tgataaaacc agctcagtag 1877
 ccctttaata agcagtggac 1897

<210> 133
 <211> 299
 <212> PRT
 <213> Bacillus licheniformis

<400> 133

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 35 40 45
 Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu Glu Ile Val Arg Glu
 50 55 60
 Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu Thr Arg Met Lys Glu
 65 70 75 80
 Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu Leu His Asp Lys His
 85 90 95
 Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln Gln Gln Tyr Phe His
 100 105 110
 Met Pro Gly Arg Val Leu His Leu Asp Gly Asp Ser Ala Tyr Leu Lys
 115 120 125
 Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val Pro Val Tyr Gly Ile
 130 135 140
 His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile Glu Glu Leu Ile Asp
 145 150 155 160
 Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly His Asp Ala Tyr Ser
 165 170 175
 Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala Tyr Arg His Ser Lys
 180 185 190
 Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg Lys Ile Pro His Leu
 195 200 205

10295.204.ST25.txt

Ala Met Arg Asn Glu Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly
 60 65 70 75

tat cat caa taaaccaggg cgacctgggt tttttgcatg aagcccgtcc 774
 Tyr His Gln

gtcgtgtttt tgcccattgt atatgctaga attggattaa atacatttgt ggaaaagggg 834
 gtagagggga aatttgtacg tctcaaaaaa agaaatagaa gtccgctatg ccgaaacaga 894
 cccaaaatgg ggtgtcgtct atcacgccaa ttatttgatt ttgggatggg aggtaagccc 954
 ggacggcttt aattaaagaa ctcggctttt ctttatgccg aaatgggaga aagacg 1010

<210> 135
 <211> 78
 <212> PRT
 <213> Bacillus licheniformis

<400> 135

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Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu Asn Ile Glu Glu Ser
 20 25 30

Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu Gln Glu Gln Ile Arg
 35 40 45

Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu Ala Met Arg Asn Glu
 50 55 60

Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly Tyr His Gln
 65 70 75

<210> 136
 <211> 2407
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1907)

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 gcaaatacg aactaacctc aagaaggcag ctgtcaaacc gacagctgcc tcagcgtgtc 240
 gacaaaccct cgcattgctt gtcagtcctg cgcgtcgggtg ctcacgaatt ccaacattcg 300
 ctccgctccg atgctcggcc ttcttagact gcaagggttt tcaatcacgc tgaaagaagg 360
 atgacaaaat cccaaaacta agagctgttt tgggattttg tcagcaatct aaggcagctg 420

10295.204.ST25.txt

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aaccgggggg gattttgagta ttg agc ata cgg gag caa aaa gag ctg cag cgg	533
Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg	10
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gcg att gaa gaa att acg gaa atc gcg gaa gga ttc ggc ctt gat ttt	581
Ala Ile Glu Glu Ile Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe	25
15	
20	
tac ccg atg aga tat gag att tgt cct gct gaa att att tat aca ttc	629
Tyr Pro Met Arg Tyr Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe	40
30	
35	
ggt gca tac ggg atg ccg aca aga tac agc cat tgg agt ttc gga aag	677
Gly Ala Tyr Gly Met Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys	55
45	
50	
caa ttt cac aaa atg aag ctt cac tat gac ttt ggc ttg agc aaa ata	725
Gln Phe His Lys Met Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile	75
60	
65	
70	
tat gag ctt gtc att aat tca gat ccg tgt tat gcg ttt ttg ctg gac	773
Tyr Glu Leu Val Ile Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp	90
80	
85	
agc aat tca ttg att caa aat aag ctg att gtc gca cac gtc ctt gct	821
Ser Asn Ser Leu Ile Gln Asn Lys Leu Ile Val Ala His Val Leu Ala	105
95	
100	
cat tgt gat ttc ttt aaa aat aac tgc cgt ttt caa aat acg aag cgc	869
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110	
115	
gat atg gtt gaa agc atg tgc gcg aca gca gag cgg att aaa cat tat	917
Asp Met Val Glu Ser Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr	135
125	
130	
gaa acg gta cac ggt tca aaa gaa gtc gaa gca ttt ctc gat gcg gtg	965
Glu Thr Val His Gly Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val	155
140	
145	
150	
ctg gcg att gaa gaa cac att gac cct tgc ctc gtg agg ccg aag ctg	1013
Leu Ala Ile Glu Glu His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu	170
160	
165	
tcg tgg agc gta gat gat gaa gag gaa gaa gaa acc ggc gcg ccg gcc	1061
Ser Trp Ser Val Asp Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala	185
175	
180	
act cct tat gac gac ctc tgg gaa ctg gat cat aaa gga tgc aaa gag	1109
Thr Pro Tyr Asp Asp Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu	200
190	
195	
aag aag aaa agg acg aaa aaa aag ttt ccg ccg aaa ccg gaa aaa gac	1157
Lys Lys Lys Arg Thr Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp	215
205	
210	
att ctg ctg ttc ata gaa gag cat tgc gcg gag ctg gag cct tgg cag	1205
Ile Leu Leu Phe Ile Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln	235
220	
225	
230	
cgc gat att tta acg atg atg aga gag gaa atg ctg tat ttc tgg ccg	1253
Arg Asp Ile Leu Thr Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro	250
240	
245	
cag ctt gaa acg aaa atc atg aat gaa ggc tgg gcg tcc tat tgg cat	1301
Gln Leu Glu Thr Lys Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His	

10295.204.ST25.txt

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ttc gcc aag ctg aac gcg gga gtg gtt cag ccg tcc aaa acg gga atc Phe Ala Lys Leu Asn Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile 285 290 295			1397
aat cct tat tat ctc gga ttg aaa ata ttt gag gac ata gag gag cgc Asn Pro Tyr Tyr Leu Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg 300 305 310 315			1445
tac aac aac ccg aca gaa gac atg aaa aag atg ggg gta gag ccg aac Tyr Asn Asn Pro Thr Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn 320 325 330			1493
tct ggg aga gaa aaa ata ttt gaa gtc agg gag atc gaa tca gac att Ser Gly Arg Glu Lys Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile 335 340 345			1541
tca ttt atc agg aac tat tta acg aag gat ctt gtg atg cgg gaa gac Ser Phe Ile Arg Asn Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp 350 355 360			1589
ctc tac ttg ttt caa aaa cag gga agg gat tat aaa atc gtc gac aag Leu Tyr Leu Phe Gln Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys 365 370 375			1637
gat tgg gag gct gtg cgc gat cag ctt gtc agc atg aga gtc aac gga Asp Trp Glu Ala Val Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly 380 385 390 395			1685
gga ttt cct tat ttg aca gtt gag gac gga gat tac tta aag aac aat Gly Phe Pro Tyr Leu Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn 400 405 410			1733
gaa tta tac atc aag cat tgg tat gaa ggg atc gaa ctc gat ttg aag Glu Leu Tyr Ile Lys His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys 415 420 425			1781
tat ctt gaa aaa gtt ctg cct tac ctc cac cag cta tgg gga aga agc Tyr Leu Glu Lys Val Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser 430 435 440			1829
gtg cat gtc gag acc gtg ctc gaa gat aaa ccc gtc atg ttt tcc tat Val His Val Glu Thr Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr 445 450 455			1877
gat gga aag gct gtc cac cgc aga tat tta taaaggctgc attttgccag Asp Gly Lys Ala Val His Arg Arg Tyr Leu 460 465			1927
ccttttttct tttaaagcgc aacgatttca actcgtccgt cctttcaaaa gaaatgccaa			1987
attaatgcac gtttgccag ttttacgact tcattataaa aatgtaaaat aaagtattta			2047
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tacctttgaa atgtaaatga aatattatct acccttaaaa actttttttg aaaacgaata			2167
attaaggaat ttgacatagt aagtcaagac tatacctgat ggaattccct ccttataata			2227
gaagcagagg aagggctgaa gcagccgttc tcaaaaaaat gaaactgcta attttcgcct			2287
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10295.204.ST25.txt

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<210> 137
 <211> 469
 <212> PRT
 <213> Bacillus licheniformis

<400> 137

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Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe Tyr Pro Met Arg Tyr
 20 25 30

Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe Gly Ala Tyr Gly Met
 35 40 45

Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys Gln Phe His Lys Met
 50 55 60

Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile Tyr Glu Leu Val Ile
 65 70 75 80

Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp Ser Asn Ser Leu Ile
 85 90 95

Gln Asn Lys Leu Ile Val Ala His Val Leu Ala His Cys Asp Phe Phe
 100 105 110

Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg Asp Met Val Glu Ser
 115 120 125

Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr Glu Thr Val His Gly
 130 135 140

Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val Leu Ala Ile Glu Glu
 145 150 155 160

His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu Ser Trp Ser Val Asp
 165 170 175

Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala Thr Pro Tyr Asp Asp
 180 185 190

Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu Lys Lys Lys Arg Thr
 195 200 205

Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp Ile Leu Leu Phe Ile
 210 215 220

Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln Arg Asp Ile Leu Thr
 225 230 235 240

10295.204.ST25.txt

Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro Gln Leu Glu Thr Lys
 245 250 255

Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His Gln Arg Ile Ile Arg
 260 265 270

Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu Phe Ala Lys Leu Asn
 275 280 285

Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile Asn Pro Tyr Tyr Leu
 290 295 300

Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg Tyr Asn Asn Pro Thr
 305 310 315 320

Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn Ser Gly Arg Glu Lys
 325 330 335

Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile Ser Phe Ile Arg Asn
 340 345 350

Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp Leu Tyr Leu Phe Gln
 355 360 365

Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys Asp Trp Glu Ala Val
 370 375 380

Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly Gly Phe Pro Tyr Leu
 385 390 395 400

Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn Glu Leu Tyr Ile Lys
 405 410 415

His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys Tyr Leu Glu Lys Val
 420 425 430

Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser Val His Val Glu Thr
 435 440 445

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His Arg Arg Tyr Leu
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<210> 138
 <211> 1291
 <212> DNA
 <213> Bacillus licheniformis

10295.204.ST25.txt

<220>

<221> CDS

<222> (501)..(791)

<400> 138

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gtgctgaaag aagcgggagc ctctctggag actgtcgtca aagcaaccgt gtttctggcg      180
gatatgaatc aattcacaga ggtgaatgaa gtttacggac agtacttcga taccacaaaa      240
ccggcgagat catgcgttga ggtggcgagg ctgccgaaag acgcgcttgt tgaaatagaa      300
gtcatcgcat tagtgaaata gaaagaactc ttaaaagatg gttttggtct caaaatcatc      360
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ggaaaagggtg gtgaactact gtg gaa gtt acc gac gta aga tta cgc cgc gtg      533
                        Val Glu Val Thr Asp Val Arg Leu Arg Arg Val
                        1          5          10

aat acc gat ggt cgc atg aga gcg att gca tcc atc acg ctg gat cac      581
Asn Thr Asp Gly Arg Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His
                        15          20          25

gaa ttt gta gtg cat gat att cgt gta att gat gga aac aat ggt ctt      629
Glu Phe Val Val His Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu
                        30          35          40

ttc gtt gcg atg cca agt aag cgt aca cct gat gga gaa ttt cgt gat      677
Phe Val Ala Met Pro Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp
                        45          50          55

atc gct cat cca atc aac tca agc acc cgc gga aaa att cag gac gcg      725
Ile Ala His Pro Ile Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala
                        60          65          70          75

gtg tta aat gaa tat cat cgt ttg ggt gac gtt gag gaa ata gaa tat      773
Val Leu Asn Glu Tyr His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr
                        80          85          90

gaa gaa att gga gct tct taaaaaagaa gggcttatgg ataagccctt      821
Glu Glu Ile Gly Ala Ser
                        95

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gtataacagt agcaggaagg taaagcatgc gaactcggat aacaaagcgc atgcagaagg      941
aatcaatccg tctccctgat cagttaatcc taaatatgct ctaaacatcc aaaatatgct      1001
gtcttgattt cccgatttct cattttggct tgcttgaaat caactcatat ttaggatata      1061
tttttctatg gataataggg ataatggagg ccaatacatg gataagcggg ttgcagttgt      1121
gttagcagct ggtcaaggaa caagaatgaa atcaaagcta tataaagttc ttcacctctg      1181
ttgcggaaaa cctatggctg agcatgttgt cgatgaagct cgcaagctat cattagaaaa      1241
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<210> 139

<211> 97

10295.204.ST25.txt

<212> PRT
 <213> Bacillus licheniformis

<400> 139

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 20 25 30

Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu Phe Val Ala Met Pro
 35 40 45

Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp Ile Ala His Pro Ile
 50 55 60

Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala Val Leu Asn Glu Tyr
 65 70 75 80

His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr Glu Glu Ile Gly Ala
 85 90 95

Ser

<210> 140
 <211> 1694
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1451)

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 aacgctgatt gatgccatca accaaaaaat taaaaaatac aacctcacct gtccgaacca 180
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 aaaagcggag atctggagct ttg ttt tca gct gtt gga cta tcg ctg caa att 533
 Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile
 1 5 10
 gat gat gga gca gtt tca gaa tca gcc gag ctt ttc cgg aaa att aaa 581
 Asp Asp Gly Ala Val Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys
 15 20 25

10295.204.ST25.txt

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 Arg Gln Lys Glu Thr Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr
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ttt ttc ttt ttt tca ggc atg tat gag ttt tat gag aaa aac tat ttt 677
 Phe Phe Phe Phe Ser Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe
 45 50 55

gag gcg atc agc tgt tac aag aaa gcg gaa gcg aag ctg cat aaa ctg 725
 Glu Ala Ile Ser Cys Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu
 60 65 70 75

acc gat gaa att gaa aaa gcg gaa ttt tat tat aaa atc gcg acc gcc 773
 Thr Asp Glu Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala
 80 85 90

tac tac caa ata gac gat cat ttc aga tcg ttg aac tac tcc gaa aaa 821
 Tyr Tyr Gln Ile Asp Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys
 95 100 105

gcg ctc tca ctt ttc agc aag cat aaa gaa tac ata gac aaa acg atc 869
 Ala Leu Ser Leu Phe Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile
 110 115 120

gga tgc gaa atg ata ctc gga tcg gtg cag ttt gaa ttg ttc cgc atc 917
 Gly Cys Glu Met Ile Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile
 125 130 135

aaa caa gct gag gag cac tac ggg cgg gcg ctt gat cag gcc gtt gcc 965
 Lys Gln Ala Glu Glu His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala
 140 145 150 155

ctt caa aac cgg cga atc atc ggg ctg atc tat cat aat atg gga ctg 1013
 Leu Gln Asn Arg Arg Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu
 160 165 170

aac tat gcc aaa tgc ggc atg ccg ctt ttg gcg gag gag cac ttt aga 1061
 Asn Tyr Ala Lys Cys Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg
 175 180 185

aaa gcc ctt tca atc ggt gtc cat gag caa tcg gtt ttt ggc att aac 1109
 Lys Ala Leu Ser Ile Gly Val His Glu Gln Ser Val Phe Gly Ile Asn
 190 195 200

acc ctt ttc gag ctg tct cac ctc atg tac aaa aac ggt tct ccc gaa 1157
 Thr Leu Phe Glu Leu Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu
 205 210 215

gaa gcg aga cgt ctc tgc aaa gag gga ttt acc aga tcg gcc gaa tta 1205
 Glu Ala Arg Arg Leu Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu
 220 225 230 235

gga gag gat gaa tac gca gcg aag ttc agg ctg att ttc gcc ctg tat 1253
 Gly Glu Asp Glu Tyr Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr
 240 245 250

gac gct ggc cat ccg ctc gat att gaa ttt tcg ctt gaa tat atg agt 1301
 Asp Ala Gly His Pro Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser
 255 260 265

gat aaa cgg cta tgg ccg cat gtt gct gaa ctg aca aaa gat att gcc 1349
 Asp Lys Arg Leu Trp Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala
 270 275 280

gac tat tac atg aag tca ggc gac cat gaa aaa agc gcg ctt tac ctg 1397
 Asp Tyr Tyr Met Lys Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu
 285 290 295

10295.204.ST25.txt

gaa aaa tcg cag cat gcg aaa aat caa ata tat aaa atg aag gag ggg 1445
 Glu Lys Ser Gln His Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly
 300 305 310 315

att ata tgaaaaaaaa catttgtttt ttccgctgca tgcttgtttg cctgatgggg 1501
 Ile Ile

ggaagcttca cagctgattc tgcagcacag gacggatcgt ttcagccatt gggaaagtcg 1561

gtgtttcctg ccagcggacg atagagataa cttgccgaga tagaaatggc ctcccgtctt 1621

ttgctatcat cgtctcacct gaaggcaatt gaagggagca gtagtgatgc cgataaaaga 1681

gatttcgcgc tgc 1694

<210> 141

<211> 317

<212> PRT

<213> Bacillus licheniformis

<400> 141

Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile Asp Asp Gly Ala Val
 1 5 10 15

Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys Arg Gln Lys Glu Thr
 20 25 30

Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr Phe Phe Phe Phe Ser
 35 40 45

Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe Glu Ala Ile Ser Cys
 50 55 60

Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu Thr Asp Glu Ile Glu
 65 70 75 80

Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala Tyr Tyr Gln Ile Asp
 85 90 95

Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys Ala Leu Ser Leu Phe
 100 105 110

Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile Gly Cys Glu Met Ile
 115 120 125

Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile Lys Gln Ala Glu Glu
 130 135 140

His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala Leu Gln Asn Arg Arg
 145 150 155 160

Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu Asn Tyr Ala Lys Cys
 165 170 175

10295.204.ST25.txt

Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg Lys Ala Leu Ser Ile
 180 185 190

Gly Val His Glu Gln Ser Val Phe Gly Ile Asn Thr Leu Phe Glu Leu
 195 200 205

Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu Glu Ala Arg Arg Leu
 210 215 220

Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu Gly Glu Asp Glu Tyr
 225 230 235 240

Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr Asp Ala Gly His Pro
 245 250 255

Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser Asp Lys Arg Leu Trp
 260 265 270

Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala Asp Tyr Tyr Met Lys
 275 280 285

Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu Glu Lys Ser Gln His
 290 295 300

Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly Ile Ile
 305 310 315

<210> 142
 <211> 1260
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1244)

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 actcaaaatc gtgttccttc gggagtgtcg gttcgacccc gaccaccggt atcactaaac 180
 atcgtattgc caaacgatga aagagcggtc ctacaaaagg agcgctcttt ttatttattc 240
 cttatcttgg aacgaagccg taagaatttt ttcttaagga ctgcgagctc cggaagctac 300
 gggaacatac cgtgagatatt atcgaaatga gcttaatacg gtgcagaaac ttttacaaaa 360
 gcaaaaatat atctgatgat ttattatcta tttatagggc gaaaagtaaa ttattgatac 420
 aaacttcttt gcaaagattg gtaactttct gtaaaatgtt ctcatagcga tagaggcagt 480
 aaagtgtggg aggtttgaca atg aaa gca gca gcc tct gtg aac gta gcc aat 533
 Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn 10
 ctc atc aat cag tgg tat gtt cac ata aaa aag aga gat gtt tca aat 581
 Page 203

10295.204.ST25.txt

Leu Ile Asn Gln Trp Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn
15 20 25

gcc gta gaa ctt agg gac aga ata aaa ggc ctt tta aac gta atg gaa 629
Ala Val Glu Leu Arg Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu
30 35 40

gaa gat cag gat gtt ttg ctt tac ttt aat cta ctt gat tac agg ttc 677
Glu Asp Gln Asp Val Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe
45 50 55

aga gta tta atg gaa gac gtc gcg ggg gag ccg cag ctt ccg cct att 725
Arg Val Leu Met Glu Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile
60 65 70 75

gct gaa gat aag gcg aag aca gac ggt ttg tta cga tac tat tac ttt 773
Ala Glu Asp Lys Ala Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe
80 85 90

ctc ttt aaa gga atg tat gaa agt gcg agg agc aac tac tct aaa gcg 821
Leu Phe Lys Gly Met Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala
95 100 105

ctt aat tgt ttt aga gtt gcc gag cgg cag ctc gat aat gtc gaa gat 869
Leu Asn Cys Phe Arg Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp
110 115 120

gaa atc gaa aag gcc gag ttt cat tat aag ctt gga aat ctc tat tat 917
Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr
125 130 135

ttt acg aaa aca act cta ctt tct ttt cat cat ctt tca atc gcg aag 965
Phe Thr Lys Thr Thr Leu Leu Ser Phe His His Leu Ser Ile Ala Lys
140 145 150 155

agc att tat agg gct tat gaa gaa tat aag aca cag tcg ata aac tgt 1013
Ser Ile Tyr Arg Ala Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys
160 165 170

acg gtg ctg ctc gca ctc aat tat ata gac gac gga cgt tta aca aga 1061
Thr Val Leu Leu Ala Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg
175 180 185

gct gaa aat atg ctt aag agt tgc gca gaa aga ctg atc aag atg ggc 1109
Ala Glu Asn Met Leu Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly
190 195 200

gat aat cat ctg ctg gcg gct gtc tac tat gat ctc ggc ttt tta aaa 1157
Asp Asn His Leu Leu Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys
205 210 215

att caa gag gat aaa cat gaa gaa gca ctc gag tat ttc gac ctc tca 1205
Ile Gln Glu Asp Lys His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser
220 225 230 235

ttt aaa acg ggt gat atc gaa aaa aat gag ccg ggg act tagctcgata 1254
Phe Lys Thr Gly Asp Ile Glu Lys Asn Glu Pro Gly Thr
240 245

gatgta 1260

<210> 143
<211> 248
<212> PRT
<213> Bacillus licheniformis
<400> 143

10295.204.ST25.txt

Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn Leu Ile Asn Gln Trp
 1 5 10 15
 Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn Ala Val Glu Leu Arg
 20 25 30
 Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu Glu Asp Gln Asp Val
 35 40 45
 Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe Arg Val Leu Met Glu
 50 55 60
 Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile Ala Glu Asp Lys Ala
 65 70 75 80
 Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe Leu Phe Lys Gly Met
 85 90 95
 Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala Leu Asn Cys Phe Arg
 100 105 110
 Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp Glu Ile Glu Lys Ala
 115 120 125
 Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr Phe Thr Lys Thr Thr
 130 135 140
 Leu Leu Ser Phe His His Leu Ser Ile Ala Lys Ser Ile Tyr Arg Ala
 145 150 155 160
 Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys Thr Val Leu Leu Ala
 165 170 175
 Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg Ala Glu Asn Met Leu
 180 185 190
 Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly Asp Asn His Leu Leu
 195 200 205
 Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys Ile Gln Glu Asp Lys
 210 215 220
 His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser Phe Lys Thr Gly Asp
 225 230 235 240
 Ile Glu Lys Asn Glu Pro Gly Thr
 245

<210> 144
 <211> 2119
 <212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1619)

<400> 144

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ttgatactaa	aggggggtgat	cagacttcga	tttgattgca	cccgaataaa	ctttatgttt	120		
gtgtaccgca	gatataatct	attgcctatc	gatttttctaa	aaggcgtaga	aatgtatctg	180		
cggttttttc	tttagctttt	tatttcataa	aagagggttg	aatttttgctt	cctaacgatt	240		
agttatgcca	aattacatat	caacaggaaa	atataatcct	tcattctgttc	tgccttcctt	300		
cctatacttc	taaaattcac	ccaaacacgg	aaaacgaatc	atattgatta	ggccaaaaaa	360		
cctctaactt	ataaagattt	ctgagaatgt	tggtgtgaaa	aattattact	tttatgtaaa	420		
atgatgacta	tgaataaaaa	gggaattgct	attttgggtt	tttagaaaaa	ttataatctt	480		
gcgagaaagg	aagaggatat	gtg agc	gtg ata	cca tat	gat ttg	ggt gcg acg	533	
		Val Ser Val	Ile Pro Tyr	Asp Leu Val	Ala Thr			
		1	5		10			
aaa atg	aat ttt	tgg tat	aca gcc	tta.aaa	aac aat	tgg aca	ggc aag	581
Lys Met	Asn Phe	Trp Tyr	Thr Ala	Leu Lys	Asn Asn	Trp Thr	Gly Lys	
	15			20		25		
gct gag	gat act	aag aaa	gaa gtt	gaa cga	gaa tta	gaa caa	atg gaa	629
Ala Glu	Asp Thr	Lys Lys	Glu Val	Glu Arg	Glu Leu	Glu Gln	Met Glu	
	30		35		40			
caa aat	cag gat	gtg att	gtc tat	tac aac	tta ctg	ctc ttc	cgg cat	677
Gln Asn	Gln Asp	Val Ile	Val Tyr	Tyr Asn	Leu Leu	Leu Phe	Arg His	
	45		50		55			
aat ctt	caa ctt	gat tat	atg tat	tct aaa	ccc ggt	gta aat	tta aat	725
Asn Leu	Gln Leu	Asp Tyr	Met Tyr	Ser Lys	Pro Gly	Val Asn	Leu Asn	
60		65		70			75	
agt cgt	ttt gat	gag ttc	aaa aag	att cgc	gat cag	aat aat	ctg gaa	773
Ser Arg	Phe Asp	Glu Phe	Lys Lys	Ile Arg	Asp Gln	Asn Asn	Leu Glu	
	80			85			90	
gga atg	ttg gat	tat tat	tat cat	ttt ttc	gct gga	atg tat	cat ttc	821
Gly Met	Leu Asp	Tyr Tyr	Tyr His	Phe Phe	Ala Gly	Met Tyr	His Phe	
	95		100			105		
aga caa	aaa gaa	tta atc	ctt gcg	ctg aat	ttt tat	agg gat	gcc gag	869
Arg Gln	Lys Glu	Leu Ile	Ala Leu	Asn Phe	Tyr Arg	Asp Ala	Glu Glu	
	110		115		120			
aaa aaa	ctc gat	tct ttt	gat tgt	gat gaa	ctg gaa	aag gct	gaa ttt	917
Lys Lys	Leu Asp	Ser Phe	Asp Cys	Asp Glu	Leu Glu	Lys Ala	Glu Phe	
	125		130		135			
tat ttc	aag gca	tct gaa	gtg tat	tac cat	atg aaa	caa acc	atc ttt	965
Tyr Phe	Lys Ala	Ser Glu	Val Tyr	Tyr Tyr	His Met	Lys Gln	Thr Ile	
140		145		150			155	
tcg atg	aat tat	gca agt	cgt gcg	tat aac	tta ttc	aaa aag	tat gat	1013
Ser Met	Asn Tyr	Ala Ser	Arg Ala	Tyr Asn	Leu Phe	Lys Lys	Tyr Asp	
		160		165			170	

10295.204.ST25.txt

act tac ggt gag cgt cga gta caa agt cag ttt att att gca ggt aac	1061
Thr Tyr Gly Glu Arg Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn	
175 180 185	
tggt cta gat cat atg tat ccc gaa aaa gct cta cat aat tta aat aaa	1109
Trp Leu Asp His Met Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys	
190 195 200	
gag ctt aaa gag tca gag aca caa gga att ctt cat ctt atg ggt tca	1157
Glu Leu Lys Glu Ser Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser	
205 210 215	
tca cat tta aat atc gga ata tgc tac aat aaa ttg gaa gat gtc gat	1205
Ser His Leu Asn Ile Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp	
220 225 230 235	
aaa gca acc tac aat ttt caa aga gct ctg aac ctt tat aaa gag gag	1253
Lys Ala Thr Tyr Asn Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu	
240 245 250	
aag cat agt ttt ttg cca aaa aca tta ttc aac ctc gca cat gtc agg	1301
Lys His Ser Phe Leu Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg	
255 260 265	
gca aag caa ggg aag ttg tca ata act gat gac cta tac tat gaa ggc	1349
Ala Lys Gln Gly Lys Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly	
270 275 280	
aaa gag ttg gct gaa aag aac aag aat tta gat atg ctt gca aag ttt	1397
Lys Glu Leu Ala Glu Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe	
285 290 295	
gat tta ata aaa ggg ctt tat ctt tca ttt gat ctg gat atg gtt cgc	1445
Asp Leu Ile Lys Gly Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg	
300 305 310 315	
gaa tcg ttc aag ttt ttc gaa agt aaa ggc aag tat gca gac atg gag	1493
Glu Ser Phe Lys Phe Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu	
320 325 330	
gaa tac ggt ctt ata gcg gct gaa cta tta gag aaa aaa gaa aaa att	1541
Glu Tyr Gly Leu Ile Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile	
335 340 345	
cga gat gca gtg gaa ttc tac cgg ata aca gtt aat gcg aga aga caa	1589
Arg Asp Ala Val Glu Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln	
350 355 360	
att caa agg agt gct ttt cta cat gta aac taaatcgttc taggggtagt	1639
Ile Gln Arg Ser Ala Phe Leu His Val Asn	
365 370	
taaagcagca ggattttctta ctataaaaaa gaattttcccc cagcattatt aaaacctcaa	1699
attttgatta cttgattatt attttaagta atcgagaaaa gaaaggctcg tctatggcaa	1759
gctattttaaa atccagaatc gtatcttatac tgtttatttct tttggaagtg gggaccggat	1819
tcgcaatttg cgagggtgtca atggaaaatc cgaattactc ctcagcttgc gcggtcttta	1879
tcatagggttt tacgattggg gaatgcttca tgattagaaa atggtaaatt ttgatcatga	1939
cgggatactc tttaccctct tctataaaag tgggacagac agttgaaaag ccggtaaatt	1999
catagccttg tatttcaaca gtaacttctt ctatatgcgg gtttcatttt ttcatctttg	2059
cttaatacat taaatcacct cttttataca gtatttgtcc attaaagaag aacaggatct	2119

10295.204.ST25.txt

<210> 145
 <211> 373
 <212> PRT
 <213> Bacillus licheniformis

<400> 145

Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr Lys Met Asn Phe Trp
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Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys Ala Glu Asp Thr Lys
 20 25 30

Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu Gln Asn Gln Asp Val
 35 40 45

Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His Asn Leu Gln Leu Asp
 50 55 60

Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn Ser Arg Phe Asp Glu
 65 70 75 80

Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu Gly Met Leu Asp Tyr
 85 90 95

Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe Arg Gln Lys Glu Leu
 100 105 110

Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu Lys Lys Leu Asp Ser
 115 120 125

Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe Tyr Phe Lys Ala Ser
 130 135 140

Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe Ser Met Asn Tyr Ala
 145 150 155 160

Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp Thr Tyr Gly Glu Arg
 165 170 175

Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn Trp Leu Asp His Met
 180 185 190

Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys Glu Leu Lys Glu Ser
 195 200 205

Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser Ser His Leu Asn Ile
 210 215 220

Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp Lys Ala Thr Tyr Asn
 225 230 235 240

10295.204.ST25.txt

Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu Lys His Ser Phe Leu
 245 250 255

Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg Ala Lys Gln Gly Lys
 260 265 270

Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly Lys Glu Leu Ala Glu
 275 280 285

Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe Asp Leu Ile Lys Gly
 290 295 300

Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg Glu Ser Phe Lys Phe
 305 310 315 320

Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu Glu Tyr Gly Leu Ile
 325 330 335

Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile Arg Asp Ala Val Glu
 340 345 350

Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln Ile Gln Arg Ser Ala
 355 360 365

Phe Leu His Val Asn
 370

<210> 146
 <211> 1405
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(905)

<400> 146
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 gttaaaacag gtgaagggga aagattccac tagagtggat gctgggtcaat tttataact 120
 ctttatttta aaagggtttc gaggagctgt ggaagctgtt gcaggcatca ataaaagatc 180
 aatattttct ttaagttgat cattcacaaa tcgaattact tctttattag gccaagtttc 240
 attttcatgg atgcacaggg tttatccgca aattccttca aatagtaaac ccttcaagat 300
 cgcggtggac gaaatttccc ttcgagaata ctgcaggtgc ggcttgaaaa agagcatata 360
 gagattcagg cgtcttagca ggcgtctttt tgttgctgat tttattgcgg cataccgaaa 420
 attttttcac ttttcaacct attatcacc gaattatagt aatatattta caaaaatgaa 480
 ataaaaaggt ataggcggaa gtg aaa cag tta ata ccc tcg tca aaa gtc gga 533
 Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly
 1 5 10
 gtg aaa atc cac gaa tgg tat aaa atg ata aga gag ttt agc gta ccg 581
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10295.204.ST25.txt

Val Lys Ile His Glu Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro
 15 20 25
 gat gca gag gct tta aaa gaa gaa gta gag aag gaa att aat caa atg 629
 Asp Ala Glu Ala Leu Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met
 30 35 40
 gaa gaa gat cag gac tta ctc ctt tac tat cag ttg atg tgt ttt aga 677
 Glu Glu Asp Gln Asp Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg
 45 50 55
 cat caa tta atg tta gaa tat tta gaa cct act aac aaa aga aaa caa 725
 His Gln Leu Met Leu Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln
 60 65 70 75
 gga caa tca ata aac aaa ttg ttg gcc caa atc gag gag cct cga aga 773
 Gly Gln Ser Ile Asn Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg
 80 85 90
 gat tta aat ggc ctc ctt agt tac tac tca ttt ttc ttt agg ggc atg 821
 Asp Leu Asn Gly Leu Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met
 95 100 105
 tat gaa ttt gag aaa aaa cag tac atc aaa gca ata gag ttt tat cga 869
 Tyr Glu Phe Glu Lys Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg
 110 115 120
 aac gca gaa aaa cag ttg gct ctc att acg atg tta tagaacaagc 915
 Asn Ala Glu Lys Gln Leu Ala Leu Ile Thr Met Leu
 125 130 135
 cgagtttcac tttaaaatgg ctgaagcata ctacatcatg aaacagacac atgtatcata 975
 tattaagggc ctttaaaata tacaataatc atgaactcta cacagtccgt aaaatccaat 1035
 gttttattgt tatcgcggt aactatgacg atttaatgcg ccatgacaaa gccttaccac 1095
 acctggaaaa tgcacttgaa ttagcgatag agatcgacaa taaaaggctc attagttctg 1155
 cctatttttaa tatagccgac tgtcatgaat gtatgggaga cattgatgca gcagttgaat 1215
 atgctgaaaa agccgtagag attaactctaa aagaagaata taacaaccta ccacaatcat 1275
 tatattactc tactcaactt ctttttaagc agaaaaacta cgagcgcgca atcgagatat 1335
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 gaatatcttg 1405
 <210> 147
 <211> 135
 <212> PRT
 <213> Bacillus licheniformis
 <400> 147
 Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly Val Lys Ile His Glu
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 Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro Asp Ala Glu Ala Leu
 20 25 30
 Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met Glu Glu Asp Gln Asp
 35 40 45

10295.204.ST25.txt

Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg His Gln Leu Met Leu
 50 55 60

Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln Gly Gln Ser Ile Asn
 65 70 75 80

Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg Asp Leu Asn Gly Leu
 85 90 95

Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met Tyr Glu Phe Glu Lys
 100 105 110

Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg Asn Ala Glu Lys Gln
 115 120 125

Leu Ala Leu Ile Thr Met Leu
 130 135

<210> 148
 <211> 2104
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1604)

<400> 148
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 gacgatatcg gctttttgat cgcgaacca gcgtcccca accattccgc tgtgaatgcg 120
 gtaatcgatg gtatggatcat ttttaatgta gatttcatat tcccatccgt tttcatacgt 180
 atagatcata tggcttccta caaactcttt tacatcttga ttcatatgaa ccgctccttt 240
 atttgtttat tgtaatcgaa acatgttgat atttacatat ataattataa aatgccgtca 300
 aaaaagatgt caaacgaaaa tacttcctga gagatttgca caaataaaga agattgttac 360
 gattaatgtc agaattttga gttatcttag gaaattatgc caatatttag aaaagtgatt 420
 gtcaaaaaat aagcgattct gtaaaatgaa aaacaacca taaaaaggaa atgacatggg 480
 aagaaaggaa ggataaacga ttg aag aca aaa att gcg tat gag gaa gtt gcg 533
 Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala
 1 5 10
 gga atg ctt aat caa tgg tat gtc atg atc aag cgt cac gaa gta tca 581
 Gly Met Leu Asn Gln Trp Tyr Val Met Ile Lys Arg His Glu Val Ser
 15 20 25
 caa gcg gtc tgc att aaa tgc gac att gag cac cag ctg ccg aat atg 629
 Gln Ala Val Ser Ile Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met
 30 35 40
 gaa gaa aat caa gat ctg ctt ctt tat ttt aat ctt tta gac tat cgg 677
 Glu Glu Asn Gln Asp Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg
 45 50 55

10295.204.ST25.txt

cac aag ctg ctg aca gaa gag ttt gcc gct tcc aac aaa ctg ttc gag His Lys Leu Leu Thr Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu 60 65 70 75	725
gat att cag gag caa aaa gcc gat atg caa agc aca gat gac atg att Asp Ile Gln Glu Gln Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile 80 85 90	773
gaa tat tat tat ttc ttt ttc gct ggc atg tac gaa ttt cat aag aag Glu Tyr Tyr Tyr Phe Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys 95 100 105	821
gat tat aca aat gca atc aat tat tat aaa tta gcc gag gaa aag ctc Asp Tyr Thr Asn Ala Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu 110 115 120	869
agg aca atc ccc gat caa atc gaa atc gcc gaa ttc cat tac aaa ctg Arg Thr Ile Pro Asp Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu 125 130 135	917
gct atc gcc tac tat caa atc aaa caa aat ttc ctt tcc tta aac cat Ala Ile Ala Tyr Tyr Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His 140 145 150 155	965
gcg aaa aca gct cta aaa acc ttc aaa gca cat gat gat tac att caa Ala Lys Thr Ala Leu Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln 160 165 170	1013
aaa gcg atc agc aac gat atg ctg atc ggg gca aat aaa ctc gat tta Lys Ala Ile Ser Asn Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu 175 180 185	1061
ttt cgt ttt gat gaa gcc gaa cag cat tac aag caa gcc ctt aaa gac Phe Arg Phe Asp Glu Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp 190 195 200	1109
gcg gca ctg atc aaa cat cat gtc ctc ctc ggc atg gct cac cac aac Ala Ala Leu Ile Lys His His Val Leu Leu Gly Met Ala His His Asn 205 210 215	1157
tta ggg ttg agc tat gtc aat cgc aac ctc ctc aca ttg gct gaa cat Leu Gly Leu Ser Tyr Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His 220 225 230 235	1205
cat ttc aaa gaa gcg ctg ctt atc aaa gag cat gaa gaa tcg gtt tac His Phe Lys Glu Ala Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr 240 245 250	1253
ggc atc cat tcc atg ttt gaa ctg aca cat gtg ctg tac aaa tca aat Gly Ile His Ser Met Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn 255 260 265	1301
gtt gtc aaa gaa gca cgc aaa ttg tat gaa aaa gga ttt ttc cgt gcg Val Val Lys Glu Ala Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala 270 275 280	1349
gaa aaa gca gga gaa agg gaa tat ttg tcg aaa ttt aaa ctt att cat Glu Lys Ala Gly Glu Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His 285 290 295	1397
gct ctg tat gat gaa cag gat cca ctt acg gtt gaa cat gct tta gaa Ala Leu Tyr Asp Glu Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu 300 305 310 315	1445
tat ctt aaa acg atc aat ctc tgg acg gat gta gcg gaa tta aca ttt Tyr Leu Lys Thr Ile Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe 320 330	1493

10295.204.ST25.txt

gat atc gca ctt tac tat aaa gaa aat gga gat gca gac aaa gct gcc 1541
 Asp Ile Ala Leu Tyr Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala
 335 340 345

gaa tat ttt gaa gaa tct cat cat gca aga gac caa att ctt aaa aga 1589
 Glu Tyr Phe Glu Glu Ser His His Ala Arg Asp Gln Ile Leu Lys Arg
 350 355 360

acg gag gag tta aag tgaaaaagat gattgccgtt gcgttgactg ccgtctttgc 1644
 Thr Glu Glu Leu Lys
 365

aagccttgctc gttttaagtt tttcgtctca gccgaaggga gatgccgagt ttgccggccg 1704

agccattttt cttgacgata agccggctca gctgatggcg ggcagagcga tctttctcga 1764

cagctttgac ggaaattcgc cagccgcctg acaaaacacc gcataaccct gcttgtcacc 1824

ggacaagctc tcttcgaaaa gcgccgccag cggcgctttt tttatgaaag caaatataac 1884

cggcgctcctt gcaaatacgtc tgcgaagatt aaaaatatga aacacatgac aggaatggcg 1944

ctcaccggct tttggctgaa tcctattgaa aaatctgccc gatttatagt gcttgtcatt 2004

ctataaatcc ttataatggt cttaacgcca atgtgaggca tgccaataga cagattgcag 2064

gggaaattct atactgaaca gcgcaattta gcatgtaatc 2104

<210> 149
 <211> 368
 <212> PRT
 <213> Bacillus licheniformis

<400> 149

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Trp Tyr Val Met Ile Lys Arg His Glu Val Ser Gln Ala Val Ser Ile
 20 25 30

Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met Glu Glu Asn Gln Asp
 35 40 45

Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg His Lys Leu Leu Thr
 50 55 60

Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu Asp Ile Gln Glu Gln
 65 70 75 80

Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile Glu Tyr Tyr Tyr Phe
 85 90 95

Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys Asp Tyr Thr Asn Ala
 100 105 110

Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu Arg Thr Ile Pro Asp
 115 120 125

10295.204.ST25.txt

Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu Ala Ile Ala Tyr Tyr
 130 135 140

Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His Ala Lys Thr Ala Leu
 145 150 155 160

Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln Lys Ala Ile Ser Asn
 165 170 175

Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu Phe Arg Phe Asp Glu
 180 185 190

Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp Ala Ala Leu Ile Lys
 195 200 205

His His Val Leu Leu Gly Met Ala His His Asn Leu Gly Leu Ser Tyr
 210 215 220

Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His His Phe Lys Glu Ala
 225 230 235 240

Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr Gly Ile His Ser Met
 245 250 255

Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn Val Val Lys Glu Ala
 260 265 270

Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala Glu Lys Ala Gly Glu
 275 280 285

Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His Ala Leu Tyr Asp Glu
 290 295 300

Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu Tyr Leu Lys Thr Ile
 305 310 315 320

Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe Asp Ile Ala Leu Tyr
 325 330 335

Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala Glu Tyr Phe Glu Glu
 340 345 350

Ser His His Ala Arg Asp Gln Ile Leu Lys Arg Thr Glu Glu Leu Lys
 355 360 365

<210> 150
 <211> 1381
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS

10295.204.ST25.txt

<222> (501)..(881)

<400> 150

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cagaggcttt aaaagaagaa gtagagaagg aaattaatca aatggaagaa gatcaggact      180
tactccttta ctatcagttg atgtgtttta gacatcaatt aatgttagaa tatttagaac      240
ctactaacia aagaaaacia ggacaatcaa taaacaaatt gttggcccaa atcgaggagc      300
ctcgaagaga tttaaatggc ctccttagtt actactcatt tttctttagg ggcattgtatg      360
aatttgagaa aaaacagtac atcaaagcaa tagagtttta tcgaaacgca gaaaaacagt      420
tggctctcat tacgatgtta tagaacaagc cgagtttcac tttaaaatgg ctgaagcata      480
ctacatcatg aaacagacac atg tat cat ata tta agg gcc ttt aaa ata tac      533
                        Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr
                        1         5         10

aat aat cat gaa ctc tac aca gtc cgt aaa atc caa tgt tta ttt gtt      581
Asn Asn His Glu Leu Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val
                        15         20         25

atc gcg ggt aac tat gac gat tta atg cgc cat gac aaa gcc tta ccc      629
Ile Ala Gly Asn Tyr Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro
                        30         35         40

cac ctg gaa aat gca ctt gaa tta gcg ata gag atc gac aat aaa agg      677
His Leu Glu Asn Ala Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg
                        45         50         55

ctc att agt tct gcc tat ttt aat ata gcc gac tgt cat gaa tgt atg      725
Leu Ile Ser Ser Ala Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met
                        60         65         70         75

gga gac att gat gca gca gtt gaa tat gct gaa aaa gcc gta gag att      773
Gly Asp Ile Asp Ala Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile
                        80         85         90

aat cta aaa gaa gaa tat aac aac cta cca caa tca tta tat tac tct      821
Asn Leu Lys Glu Glu Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser
                        95         100         105

act caa ctt ctt ttt aag cag aaa aac tac gag cgc gca atc gag ata      869
Thr Gln Leu Leu Phe Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile
                        110         115         120

ttt ctt att ggt tagacaaaca gctcgaaaat tcaacgatac cctattcact      921
Phe Leu Ile Gly

tctctatttg aatatcttga ggcgttatat atctattctg tgaataaaga agagatttta      981
gaggatattta aatacttggg ggagaataaa atatttgcat acatagaaga gctttcgctt      1041
gaagtctcta accaatacct tgaaagaaaa gaccatagaa actcaatcga gttccttcaa      1101
aaaatgatgt atgggcaaac aaaaattaaa aaaggggagt gtctctatga gtattaaaaa      1161
gctcgttatt cccatttttag ccgccgcgtt attaacgatg ggtattagcg ttgtttcagc      1221
aaccgaccag tctgacggcg tatatcaaat cgctacccgt aagcaaactg aagaaacgcc      1281
ccaaatgtgg ggcgcttttt atttctacgg tttcttaacg ttaaactcgc tgattaactt      1341

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10295.204.ST25.txt

1381

cttatcagct gtcggttaaga ttaacgtata ccattccgac

<210> 151
 <211> 127
 <212> PRT
 <213> Bacillus licheniformis

<400> 151

Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr Asn Asn His Glu Leu
 1 5 10 15

Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val Ile Ala Gly Asn Tyr
 20 25 30

Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro His Leu Glu Asn Ala
 35 40 45

Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg Leu Ile Ser Ser Ala
 50 55 60

Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met Gly Asp Ile Asp Ala
 65 70 75 80

Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile Asn Leu Lys Glu Glu
 85 90 95

Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser Thr Gln Leu Leu Phe
 100 105 110

Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile Phe Leu Ile Gly
 115 120 125

<210> 152
 <211> 1735
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1235)

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 tcgcagacgc cgtattcagc ggggactccg gccgttttgc gcgcatctat cttgaaaagc 180
 ttctgcacgc tccgctggca gcgatgattg agacaaaaaa gatctatcag gcgttgaatg 240
 gaggcaggct gcagaaaacg cttgaactcg agaaaacggc ccagatgaaa atgaggctga 300
 caagcgacca tcaggaaggg atccgcgcat ttttagaaaa gcgccagccg caatttaacc 360
 gtcagcaagt ataacaagag cgggtccggca ggaaattgac cttgggaaat gatgtgcaga 420

10295.204.ST25.txt

aacaattgta aaaaaattta agtttccata aaatgattca taagatacag atctgtacga 480
agtccttggga ggcggcgaaa ttg aaa cag aag att cca tct gaa tac gtt gct 533
Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala
1 5 10
aga aag ctg aat gat tgg tac aac gcc att cgg aaa aat cag atc gcc 581
Arg Lys Leu Asn Asp Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala
15 20 25
gcc agt gaa tca ttg aaa gcg gaa att tta aat gat ttt caa gac atg 629
Ala Ser Glu Ser Leu Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met
30 35 40
gaa gaa aat cgg gac gtc ctg ctc tac tat tcg ctg ctt gaa ttc agg 677
Glu Glu Asn Arg Asp Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg
45 50 55
cat aaa ctg atg ctc agc tat ttg aaa ccg aaa gag act gaa aat att 725
His Lys Leu Met Leu Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile
60 65 70 75
gaa aaa aac ctc cgc gac tta gaa gaa aaa gaa gac caa atg acg ggt 773
Glu Lys Asn Leu Arg Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly
80 85 90
tta tta aac tat tat tac tgg ttt ttt aaa ggg atg tat gag ttc aaa 821
Leu Leu Asn Tyr Tyr Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys
95 100 105
caa aag cgg ttc gtc aaa gca atc ggc tgc tat aaa acg gct gaa caa 869
Gln Lys Arg Phe Val Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln
110 115 120
aaa gtc agc gca ctg gaa gac gag gtt gaa aaa gcg gaa ttt tat tat 917
Lys Val Ser Ala Leu Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr
125 130 135
aag ctt gcg gaa atc tac tat tat atc aac cag aga tac ctg tcg atc 965
Lys Leu Ala Glu Ile Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile
140 145 150 155
aac tat gcg acg cta gct tcc gac att ttt aac cgg tat gaa acg cta 1013
Asn Tyr Ala Thr Leu Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu
160 165 170
aaa gaa aaa aag att ttc tgc gat ttt atc att gcc ggt aat tgg gtt 1061
Lys Glu Lys Lys Ile Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val
175 180 185
gaa tcg atg aca tac gga ccc gcg ctg aaa agc ctg gcc aat gcg ctt 1109
Glu Ser Met Thr Tyr Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu
190 195 200
gaa gac gcc agg aaa atc aaa aac agc cat ttg acg gca gcc gct cat 1157
Glu Asp Ala Arg Lys Ile Lys Asn Ser His Leu Thr Ala Ala Ala His
205 210 215
ttt aat ttg gga aat tgc tat ttc cac caa gaa tcg tac cgg gaa gcc 1205
Phe Asn Leu Gly Asn Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala
220 225 230 235
tca gat cat atg gag cgc cct ttc cat ttt tgaacaggaa agttcatcat 1255
Ser Asp His Met Glu Arg Pro Phe His Phe
240 245
atattcccaa agtgctgtac aacttgatgt acgtccgtct caagcagggg aacctgccc 1315

10295.204.ST25.txt

gagctgccgc ctgttatgaa aaaggcatcc gaagcgcggc atcgctcggg gatgaagaac 1375
 acgcggcaaa gcttaacatt ctgtgcgggc tgtatttaga cggaggggat cagaaagccg 1435
 tggaaaacgg atttgattat ttggagtcaa atcatttata tgctgctgtt gaagagctgg 1495
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 atgaaaagtg cgctcaggca agtcgaaaaa tcaaaagggg agatgcgttg tatgaaagct 1615
 aaactgttgt tcgtcgcggg gtcgctggct gttgtgttaa cgtcttcaag ctttttggca 1675
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<210> 153
 <211> 245
 <212> PRT
 <213> Bacillus licheniformis

<400> 153

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 20 25 30

Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met Glu Glu Asn Arg Asp
 35 40 45

Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg His Lys Leu Met Leu
 50 55 60

Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile Glu Lys Asn Leu Arg
 65 70 75 80

Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly Leu Leu Asn Tyr Tyr
 85 90 95

Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys Gln Lys Arg Phe Val
 100 105 110

Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln Lys Val Ser Ala Leu
 115 120 125

Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr Lys Leu Ala Glu Ile
 130 135 140

Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile Asn Tyr Ala Thr Leu
 145 150 155 160

Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu Lys Glu Lys Lys Ile
 165 170 175

Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val Glu Ser Met Thr Tyr
 180 185 190

10295.204.ST25.txt

Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu Glu Asp Ala Arg Lys
 195 200 205

Ile Lys Asn Ser His Leu Thr Ala Ala Ala His Phe Asn Leu Gly Asn
 210 215 220

Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala Ser Asp His Met Glu
 225 230 235 240

Arg Pro Phe His Phe
 245

<210> 154
 <211> 2116
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1616)

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 tctcctctaa tccttttcat tacaatcagt atatagttta ccactttata gaaagtactt 240
 ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat 300
 tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa 360
 accaaaaagc catttgtttt aaattgggtct ttcgggtatca cgaaaatttc gttttttggg 420
 ctgatagaag ttttgcaatt atgaattgta tgtaaatctt taacataaaa aggatgtag 480
 ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc 533
 Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
 1 5 10
 aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa 581
 Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
 15 20 25
 gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629
 Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
 30 35 40
 gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat 677
 Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His
 45 50 55
 gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa 725
 Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys
 60 65 70 75
 tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc 773
 Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly
 80 85 90

10295.204.ST25.txt

ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct	821
Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser	
	95 100 105
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa	869
Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys	
	110 115 120
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat	917
Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr	
	125 130 135
aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg	965
Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met	
	140 145 150 155
tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat	1013
Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr	
	160 165 170
gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att	1061
Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile	
	175 180 185
gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag	1109
Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys	
	190 195 200
gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt	1157
Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu	
	205 210 215
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct	1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala	
	220 225 230 235
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca	1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala	
	240 245 250
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga	1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg	
	255 260 265
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa	1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu	
	270 275 280
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt	1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val	
	285 290 295
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa	1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu	
	300 305 310 315
aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa	1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu	
	320 325 330
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat	1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn	
	335 340 345
gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc	1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Glu Lys Gln Ile	
	350 355 360

10295.204.ST25.txt

aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga 1636
 Lys Arg Gly Asp Phe Leu Tyr Glu Ile
 365 370
 cccttgcttt gggcttggtg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac 1696
 aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcagggtcat 1756
 gtgatggcct gccttttttg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816
 taatactcat ctttcttcgt cccttggtt ggaattttca tcatatcaat atttgaatat 1876
 gcggctgtcc gcattattaa caattttaaa ttttttgac aaattttata caaaggcaga 1936
 caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc 1996
 taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt 2056
 ttattcctca tcaaagcgga gagccgcaa cataaacgca atgaccaact gttgtccgca 2116

<210> 155
 <211> 372
 <212> PRT
 <213> Bacillus licheniformis
 <400> 155

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
 1 5 10 15

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
 20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
 35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
 50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
 65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
 85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
 100 105 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
 115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
 130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
 145 150 155 160

10295.204.ST25.txt

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
 165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
 180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
 195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
 210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
 225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
 245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
 260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
 275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
 290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
 305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
 325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
 340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
 355 360 365

Leu Tyr Glu Ile
 370

<210> 156
 <211> 1576
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1268)

<400> 156

10295.204.ST25.txt

cggagcctcc attccaaaac gagtactggg acctgcatga agacgggatac tatgtcgata	60
tcgttttcagg gaagccgctg ttttcatcgc ttgacaaatt tgacgcacac tgcggctggc	120
caagcttcac aaaaccggtc gatgccggag aaatcgaaga aaagctggac acttcacacg	180
gcatgattcg gactgagggtg agaagcaagt ctgccgattc ccattcttga cacgtgtttc	240
cggacggacc cggaccggac ggcctgcgct attgcatcaa ttcagccgcc ctccgggttg	300
tgccgaagga cgaccttgag aaagaaggat acggcgaata tgtcaaactg tttgaacgca	360
agaaatccgg agaggaaagc tgaggagagc agcatgcaag atgatacttt tttcaaagg	420
tcatacttttt ttagaggatt ttctgctctg aaagcgaaaa aacattacaa tagatcatct	480
tgagaaaaga ggcagccgtt gtg aca tcc att tca aac aca gaa gac cgt tat	533
Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr	10
1 5	
tta atg ctg aca tgc agc aaa aaa att gaa tcc cat tat cat ata tac	581
Leu Met Leu Thr Cys Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr	25
15 20	
aca gat gag gag atc ccg cag atg ttt tcc tct cat ttt ctg cag ctg	629
Thr Asp Glu Glu Ile Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu	40
30 35	
cag gac gat ttt ccg ctg aca gag ctg tac tcc ctg ctc gtt cgg aca	677
Gln Asp Asp Phe Pro Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr	55
45 50	
ccc gaa att tta aaa cga aat tat gtt cat gtg aaa agc tct tat aag	725
Pro Glu Ile Leu Lys Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys	75
60 65 70	
cgg gat ctg cct ttt acg atg aaa aag tcg ctc ttt gat ctt ggc tat	773
Arg Asp Leu Pro Phe Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr	85 90
80	
att ctt gat gaa gaa ttg ttt tat tcc atc agg ctt gca gat tgg aaa	821
Ile Leu Asp Glu Glu Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys	100 105
95	
gga gat tcc cct ggt gta cgg gca gag tgg ggg acg gag aaa tcg ctc	869
Gly Asp Ser Pro Gly Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu	110 115 120
110	
att gac ggc tgc cgc atg atg cag gct tat gat aca ttg tct atc aat	917
Ile Asp Gly Cys Arg Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn	125 130 135
125	
gaa gcg ttt gcg aag gaa aag ctg ctg cgc aag tat cct ttt tat gag	965
Glu Ala Phe Ala Lys Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu	140 145 150 155
140	
gaa ggc atc att cag ctg tgt gtc tgc tac tcg gaa gaa ggc gaa ccg	1013
Glu Gly Ile Ile Gln Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro	160 165 170
160	
att gga tgt gct gag ctt tat ctc gat cac gac gaa aac gtt gct aaa	1061
Ile Gly Cys Ala Glu Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys	175 180 185
175	
atc gaa gaa gtc gcc att ttg gag cca tac cag cgg aaa ggc tat gga	1109
Ile Glu Glu Val Ala Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly	190 195 200
190	

10295.204.ST25.txt

tcg ggc ctt atc aag cag atg ctc acc gcc gcc aaa caa tcg ggc atg	1157
Ser Gly Leu Ile Lys Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met	
205 210 215	
gaa tcg tgc tat ctt gta act tcg gga agc gat cag gtg aaa acg ttt	1205
Glu Ser Cys Tyr Leu Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe	
220 225 230 235	
tat gaa aag ctg ggc ttt cag cag aag gaa aag ctc acg aca ata ttt	1253
Tyr Glu Lys Leu Gly Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe	
240 245 250	
aaa tat ttg ttc gta taaagtaggc aggtgcacat accaattggg acttggcctg	1308
Lys Tyr Leu Phe Val	
255	
cataggctgg ggtgtagact ttatacgaaa ggatgataag cctgtgcatt actcccatta	1368
ttgctgtcct actggaggat acggctacgg gtttcacgga agaacacatt tgactcatcg	1428
ttgtcctctt tattttgctc atcattgtcg gtgcggcttt catttgctag ctaaaagccc	1488
gacgcccggc gcttgacatg ctcacaaagc cttcctccgg aagggtttttt ttgggttttg	1548
ttggaaaatt ttgcattcgt atgtaata	1576

<210> 157
 <211> 256
 <212> PRT
 <213> Bacillus licheniformis

<400> 157

Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr Leu Met Leu Thr Cys
 1 5 10 15

Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr Thr Asp Glu Glu Ile
 20 25 30

Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu Gln Asp Asp Phe Pro
 35 40 45

Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr Pro Glu Ile Leu Lys
 50 55 60

Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys Arg Asp Leu Pro Phe
 65 70 75 80

Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr Ile Leu Asp Glu Glu
 85 90 95

Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys Gly Asp Ser Pro Gly
 100 105 110

Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu Ile Asp Gly Cys Arg
 115 120 125

Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn Glu Ala Phe Ala Lys
 130 135 140

10295.204.ST25.txt

Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu Glu Gly Ile Ile Gln
 145 150 155 160

Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro Ile Gly Cys Ala Glu
 165 170 175

Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys Ile Glu Glu Val Ala
 180 185 190

Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly Ser Gly Leu Ile Lys
 195 200 205

Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met Glu Ser Cys Tyr Leu
 210 215 220

Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe Tyr Glu Lys Leu Gly
 225 230 235 240

Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe Lys Tyr Leu Phe Val
 245 250 255

<210> 158
 <211> 1783
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1283)

<400> 158
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 ttgagtttct ttttactttt ttcgatcagc tcgtcttcat caggagctga cagcggacga 120
 ttattgacaa acgcaaacga tttttttcgt cccggcccg c agtaagactg gcagccgatt 180
 tccacttttg catccggatc aatttctttc agacggggca aaagcgtctt taaattgggtg 240
 gcctggcaat cgtcgcatac tcgaaattca ttagccattt catacgcttc ctttcgtttt 300
 gttcatctgt ctttatgaaa ggcattcaac tgtgccgaac ttttataaaa aatgacacca 360
 tccttcattt tacaaggatt ctttcattcc tgcaaggatc gcgctaaaaa aatcagttcc 420
 tattctttta gcaaacttgt ataaatattt tccaaaatgg acaatctaata accaataactg 480
 acaatgggag ttgagaagtg atg aaa caa aga caa gac gct tgg tct gag gaa 533
 Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu
 1 5 10
 aat gat tta ctg ctt gct gaa acg gta ttg cgg cat gtc agg gaa ggg 581
 Asn Asp Leu Leu Leu Ala Glu Thr Val Leu Arg His Val Arg Glu Gly
 15 20 25
 agc aca cag ctg aac gcc ttc gag gaa gtc gga gac aga ctg aac agg 629
 Ser Thr Gln Leu Asn Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg
 30 35 40

10295.204.ST25.txt

aca tca gcc gcc tgc ggt ttt aga tgg aac gca gtt gtc cgc cac caa 677
 Thr Ser Ala Ala Cys Gly Phe Arg Trp Asn Ala Val Val Arg His Gln
 45 50 55
 tac gaa aaa gca ttg cag ctg gct aaa aaa cag agg aag caa aga atg 725
 Tyr Glu Lys Ala Leu Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met
 60 65 70 75
 cgc gcc ctc gga aac gga cag ccg gcg aaa aaa cgc tta tta tac aag 773
 Arg Ala Leu Gly Asn Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys
 80 85 90
 ccg ccg gtc gaa acg aat gct gaa cct cct gca gaa agc gtt gtt gag 821
 Pro Pro Val Glu Thr Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu
 95 100 105
 cag aag aaa gca acc gca gat tca agc gaa cag cag ccg atc gcc agc 869
 Gln Lys Lys Ala Thr Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser
 110 115 120
 gag cat ctg cct tat gtt gat gag agc ttt aaa gaa gag tta gct agt 917
 Glu His Leu Pro Tyr Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser
 125 130 135
 tta tct cac ctt cta tcg cca aat cag ccg cag gcc ggc cat aca gcc 965
 Leu Ser His Leu Leu Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala
 140 145 150 155
 gat aca tcg aaa gac atg acg atc gat gat gtg atc cgc ttc ctg caa 1013
 Asp Thr Ser Lys Asp Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln
 160 165 170
 aac tat aca gga aac gaa gaa caa act gcc gct tta aaa atg gaa aat 1061
 Asn Tyr Thr Gly Asn Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn
 175 180 185
 gaa cgt tta aaa cag gaa aac gaa gaa ctg acg aag aaa gtt gaa aag 1109
 Glu Arg Leu Lys Gln Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys
 190 195 200
 ctt gaa gcg gaa gtc aaa aag ctg gaa aaa gac cag aca acc atc cag 1157
 Leu Glu Ala Glu Val Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln
 205 210 215
 gaa gac tac gaa acg ctc gta aaa att atg aac cgt gca aga aaa cta 1205
 Glu Asp Tyr Glu Thr Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu
 220 225 230 235
 gtt tta ttc gaa gaa gac gaa cac gct gcg ccc gcc ttc aaa atg gac 1253
 Val Leu Phe Glu Glu Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp
 240 245 250
 cgg aac ggc aat tta gaa aaa atg gct gaa tagcgcctctc agaggatgcg 1303
 Arg Asn Gly Asn Leu Glu Lys Met Ala Glu
 255 260
 gcagagacgt tcaggcagca aggactgaca atgcatacaa acatttttctg atacgaggat 1363
 acccctttct ttaaaaaagg ggggtattttt acctttctgc ggcttgcttt tatatgacaa 1423
 aaatttcata atagggatag caattcataa ggcgggggtat tcgatgaagt ttgttttata 1483
 tgcggttcag ttcggcactg cggccctttt gtttttgttt tctgcattgg caagctggta 1543
 tcaaggcagc gagcttttaa aggtgccgtg ggagtggaaa tatacagcca agtttacaag 1603
 ttggctgtac ggagaggact ccattaaaaa cgcacataat atttcacagc ttgatttttt 1663

10295.204.ST25.txt

cgctctatgcg gccaaagcata cgccggcaac cgttatttta atggccgtca gtttggcgta 1723
 tatcatcgct ttggcggtt atcttctcat caaaacatat gtaaacgaa aaagcgcttc 1783

<210> 159
 <211> 261
 <212> PRT
 <213> Bacillus licheniformis

<400> 159

Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu Asn Asp Leu Leu Leu
 1 5 10 15

Ala Glu Thr Val Leu Arg His Val Arg Glu Gly Ser Thr Gln Leu Asn
 20 25 30

Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg Thr Ser Ala Ala Cys
 35 40 45

Gly Phe Arg Trp Asn Ala Val Val Arg His Gln Tyr Glu Lys Ala Leu
 50 55 60

Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met Arg Ala Leu Gly Asn
 65 70 75 80

Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys Pro Pro Val Glu Thr
 85 90 95

Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu Gln Lys Lys Ala Thr
 100 105 110

Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser Glu His Leu Pro Tyr
 115 120 125

Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser Leu Ser His Leu Leu
 130 135 140

Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala Asp Thr Ser Lys Asp
 145 150 155 160

Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln Asn Tyr Thr Gly Asn
 165 170 175

Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn Glu Arg Leu Lys Gln
 180 185 190

Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys Leu Glu Ala Glu Val
 195 200 205

Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln Glu Asp Tyr Glu Thr
 210 215 220

10295.204.ST25.txt

Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu Val Leu Phe Glu Glu
225 230 235 240

Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp Arg Asn Gly Asn Leu
245 250 255

Glu Lys Met Ala Glu
260

<210> 160
<211> 2311
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1811)

<400> 160
tgatgtcttc ccattcattt tcaaggctgc atagcataac gccgtcgact tctttcctct 60
tgagcagctc cagtactttc agttcattct gcttttgata aaacgtctga aacacaatga 120
ctttgtattg gtgtttcagc gcttcagcgg acatatgctt cataagctga gcgaagaagg 180
gggtggccgc gtgtgggaca gacactgcga gaaacatcgt tttgttggat ctgagctttc 240
gtgcagacgt gttcgggatg tagtccaatt tttcgaatgac ttccaaaacc cgcttccttt 300
tttcttcaga tacatagggg tgatcggtca gtactcttga aacagtgtgt tttgacacat 360
tacttaattt tgcaatttcg tcaatcgtag gcataaagtc acttcctgaa aaaaagagtt 420
gttatggtat cgattccatc atttaagata tgtcatgaaa tatgacaatt tcccaaaata 480
ataaaaaatgg ggtgaaattg atg aaa acc gca aac gaa aac atg act tgc acg 533
Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr 10
1 5 10
agc aaa cag cta ttt gtc ctt ctg aat gat ttg aag gaa gga aag ctc 581
Ser Lys Gln Leu Phe Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu 25
15 20 25
gct ggt gaa tgc cgt ata gac gac aca ctg gcc aat caa aaa tta aaa 629
Ala Gly Glu Cys Arg Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys 40
30 35 40
gag aca ttg cag cag gat caa ttc gac ata acc gcc aat ttg ctg aac 677
Glu Thr Leu Gln Gln Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn 55
45 50 55
aga atg gat tcc ccg ccc tcc aga gtt gac ttt atg ccg ctt cat cga 725
Arg Met Asp Ser Pro Pro Ser Arg Val Asp Phe Met Pro Leu His Arg 75
60 65 70 75
ctg atc aca gaa gaa gaa gta gat gac gtg gtt cat gcg gtg aaa gac 773
Leu Ile Thr Glu Glu Glu Val Asp Asp Val Val His Ala Val Lys Asp 90
80 85 90
gtg ctg ccg acc ggg caa ttt aca agc ggt ttt tat gtt ggc gta ttt 821
Val Leu Pro Thr Gly Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe 105
95 100 105

10295.204.ST25.txt

gaa gct gaa ata gct gct ttt ttg agc aaa aag cat gtc atg gct tca Glu Ala Glu Ile Ala Ala Phe Leu Ser Lys Lys His Val Met Ala Ser 110 115 120	869
tcc agc gga acc gat gcc atg att gtc gcg ctg aag gct gcg ggt gtt Ser Ser Gly Thr Asp Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val 125 130 135	917
gga caa ggt gat gaa gtc att atg cct gca aac agc ttt gct gca acg Gly Gln Gly Asp Glu Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr 140 145 150 155	965
gaa aac gcc gtg ctc gca gct gga ggc act ccg att ttc tgc gat att Glu Asn Ala Val Leu Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile 160 165 170	1013
gac cct gtt aca ttt tgc atg gat cct tca gaa att gaa gca tgt gtc Asp Pro Val Thr Phe Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val 175 180 185	1061
act ttg aaa acg aaa tgc att ttg cct gta cac ctt tat gga aag ctg Thr Leu Lys Thr Lys Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu 190 195 200	1109
cct gac atg gaa gcc att gca aaa acc gct gat aaa tac ggc atc ccg Pro Asp Met Glu Ala Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro 205 210 215	1157
att att gaa gac gcc tgc cag gcg atc ggc gtt tcc gat ctg gga aaa Ile Ile Glu Asp Ala Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys 220 225 230 235	1205
aac agc ctt tgc tcc ata tta agc ttc aat ccg tat aaa aat ctc ggc Asn Ser Leu Cys Ser Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly 240 245 250	1253
act tgc gga aaa gcc ggc gca att gtg acg gat gat cca tca ttt gca Thr Cys Gly Lys Ala Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala 255 260 265	1301
tcc gca tgc atg gaa tat atg tat cac ggc ttt gaa ctg aat caa aaa Ser Ala Cys Met Glu Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys 270 275 280	1349
aat aaa aag gcg gct gac tac ggc ttt aac gct aag att gat aat ctg Asn Lys Lys Ala Ala Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu 285 290 295	1397
caa gcc gct att gga ctg gca agg atg aaa tat ctt tct tta aat aat Gln Ala Ala Ile Gly Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn 300 305 310 315	1445
ctg aag cgc tta tat tta gca gat cgt tat att gcg cat ttg cag cag Leu Lys Arg Leu Tyr Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln 320 325 330	1493
tat gaa gac aga ggt ctg atc aaa ttg cct caa atg acc gat gat cat Tyr Glu Asp Arg Gly Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His 335 340 345	1541
gta tgg cat ttg ttt aca att aaa ata cta aac gga aat cgt gac caa Val Trp His Leu Phe Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln 350 355 360	1589
gtc aaa gat atg atg ctt aaa ttt cat aat gtc caa aca gat ata tac Val Lys Asp Met Met Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr 365 370 375	1637

10295.204.ST25.txt

tac ccg att tta tcc cat cat caa aac aca cca ctt gta aaa gcc aat 1685
 Tyr Pro Ile Leu Ser His His Gln Asn Thr Pro Leu Val Lys Ala Asn 395
 380 385 390

tat cgg cac aca tca ctg ccg gtc act gaa tca gtg cat aaa caa atg 1733
 Tyr Arg His Thr Ser Leu Pro Val Thr Glu Ser Val His Lys Gln Met 410
 400 405

ctt cag ctt cct ctc tat ccg ggg ctc acc gta gaa gaa caa gac aaa 1781
 Leu Gln Leu Pro Leu Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys 425
 415 420

gta atg gag gcc tta att gat gtc gta tca tgaaacactt tcttttcaca 1831
 Val Met Glu Ala Leu Ile Asp Val Val Ser 435
 430

ccttgcagca agtaaacaag ccgaagtacg ccgtattttg cgattttgat gagacatatt 1891
 tcgcccacag catcaccgat gaatcgagaa aagcgctcat ggaccttgaa acattttattc 1951
 attcgcacca tcttgatcac aagattttgc tcggctgggt gaccgggagc agcctgtcat 2011
 ccgttcttgc aaaaatgaag cggggaggct ttcgatatct tccgcatttt gtcgccgggtg 2071
 accttggcac tgaaatcact tatttctctg aagaaggcca agtctctgat aaagattggg 2131
 aagcccgatt gcaagaatca aatttctccc atgatctggt cgaagaaatc aagcagactc 2191
 tctctaaaaa atatgagatt gcgcttgtgc ctcagactca gcatggcttt tcccgtata 2251
 aaatcaacta ttactataaa tcgttggaag agagcataga taagagggcg cttgaagcca 2311

<210> 161
 <211> 437
 <212> PRT
 <213> Bacillus licheniformis
 <400> 161

Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr Ser Lys Gln Leu Phe
 1 5 10 15

Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu Ala Gly Glu Cys Arg
 20 25 30

Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys Glu Thr Leu Gln Gln
 35 40 45

Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn Arg Met Asp Ser Pro
 50 55 60

Pro Ser Arg Val Asp Phe Met Pro Leu His Arg Leu Ile Thr Glu Glu
 65 70 75 80

Glu Val Asp Asp Val Val His Ala Val Lys Asp Val Leu Pro Thr Gly
 85 90 95

Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe Glu Ala Glu Ile Ala
 100 105 110

10295.204.ST25.txt

Ala Phe Leu Ser Lys Lys His Val Met Ala Ser Ser Ser Gly Thr Asp
 115 120 125

Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val Gly Gln Gly Asp Glu
 130 135 140

Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr Glu Asn Ala Val Leu
 145 150 155 160

Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile Asp Pro Val Thr Phe
 165 170 175

Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val Thr Leu Lys Thr Lys
 180 185 190

Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu Pro Asp Met Glu Ala
 195 200 205

Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro Ile Ile Glu Asp Ala
 210 215 220

Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys Asn Ser Leu Cys Ser
 225 230 235 240

Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly Thr Cys Gly Lys Ala
 245 250 255

Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala Ser Ala Cys Met Glu
 260 265 270

Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys Asn Lys Lys Ala Ala
 275 280 285

Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu Gln Ala Ala Ile Gly
 290 295 300

Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn Leu Lys Arg Leu Tyr
 305 310 315 320

Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln Tyr Glu Asp Arg Gly
 325 330 335

Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His Val Trp His Leu Phe
 340 345 350

Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln Val Lys Asp Met Met
 355 360 365

Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr Tyr Pro Ile Leu Ser
 370 375 380

10295.204.ST25.txt

His His Gln Asn Thr Pro Leu Val Lys Ala Asn Tyr Arg His Thr Ser
 385 390 395 400

Leu Pro Val Thr Glu Ser Val His Lys Gln Met Leu Gln Leu Pro Leu
 405 410 415

Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys Val Met Glu Ala Leu
 420 425 430

Ile Asp Val Val Ser
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 <212> DNA
 <213> Bacillus licheniformis

<220>
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 gttttgattc atccctctgc tgttgtcagc gggtcggccc ggattcaaaa cggcgccggt 180
 gttatggcat cgagcgtcat ccaagcggat gcagacgtcg gcatccacgc gattgtcaac 240
 acaggtgcca tcgtcgaaca cgacaatcgg atcggcgatt acgttcattct ttcgcccgga 300
 acggtgttaa ccggcggcgt gacagttatg gaaggcgctc atctcggcgc gggaacggcg 360
 gtcattcccg gaaagacagt cggacgctgg agcgtgacgg gagcgggggc agccgtgatt 420
 caccgacattc ctgataattg caccgcagtc ggagtccttg caagaatgat caaataacag 480
 cagtaaaaag ggtgaaaaac atg agt cag aat aag cga att tat tta tca ccg 533
 Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro
 1 5 10
 ccg cac atg agc gga gac gag gag cgc tat gta gcc gaa gcg ttt cgg 581
 Pro His Met Ser Gly Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg
 15 20 25
 aca aac tgg atc gcg ccc ctc ggt ccc ctt gtc gac aca ttt gaa gaa 629
 Thr Asn Trp Ile Ala Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu
 30 35 40
 aag ctt gcc gcc tat gcg ggg acg tcc gga gcc gcg gca gtc agc tca 677
 Lys Leu Ala Ala Tyr Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser
 45 50 55
 gga aca gct gcg atc cac ctg gcc ttg aaa ttg ctc ggc gtc ggc aaa 725
 Gly Thr Ala Ala Ile His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys
 60 65 70 75
 ggc gat acg gtc ttc tgc tct tct ttt acg ttt gta gcg agc gcc aat 773
 Gly Asp Thr Val Phe Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn
 80 85 90
 ccg atc ata tat gag cag gct gaa ccg gtt ttc att gat tct gaa cgg 821

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Pro	Ile	Ile	Tyr	Glu	Gln	Ala	Glu	Pro	Val	Phe	Ile	Asp	Ser	Glu	Arg		
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Asp	Thr	Trp	Asn	Met	Ser	Pro	Glu	Ala	Leu	Glu	Arg	Ala	Leu	Asp	Glu		
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gcg	gag	cgg	gcc	agg	aat	ctc	ccg	aaa	gcc	gtc	atc	gtc	gtc	aac	ttg	917	
Ala	Glu	Arg	Ala	Arg	Asn	Leu	Pro	Lys	Ala	Val	Ile	Val	Val	Asn	Leu		
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tac	ggc	caa	agc	gcg	aaa	atg	gac	gag	att	atg	gcc	att	tgc	gat	cga	965	
Tyr	Gly	Gln	Ser	Ala	Lys	Met	Asp	Glu	Ile	Met	Ala	Ile	Cys	Asp	Arg		
	140				145				150						155		
ttt	gcc	gtg	cct	gtc	att	gaa	gat	gca	gcc	gaa	tcg	ctc	ggt	tct	gtt	1013	
Phe	Ala	Val	Pro	Val	Ile	Glu	Asp	Ala	Ala	Glu	Ser	Leu	Gly	Ser	Val		
				160					165					170			
tat	aaa	ggc	aga	aaa	agc	ggg	acc	ttc	gga	cgc	ttc	ggc	att	tat	tcg	1061	
Tyr	Lys	Gly	Arg	Lys	Ser	Gly	Thr	Phe	Gly	Arg	Phe	Gly	Ile	Tyr	Ser		
			175					180					185				
ttc	aac	ggt	aac	aaa	atc	atc	acc	aca	tcg	ggc	gga	gga	atg	ctg	gtc	1109	
Phe	Asn	Gly	Asn	Lys	Ile	Ile	Thr	Thr	Ser	Gly	Gly	Gly	Met	Leu	Val		
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Ser	Asp	Asp	Glu	Asp	Ala	Leu	Lys	Lys	Ala	Arg	Phe	Leu	Ala	Thr	Gln		
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Ala	Arg	Glu	Pro	Ala	Ile	His	Tyr	Gln	His	Glu	Lys	Ala	Gly	Tyr	Asn		
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tac	cgg	atg	agc	aat	gtt	ctg	gcc	gga	atc	ggc	atc	gca	cag	ctc	gcc	1253	
Tyr	Arg	Met	Ser	Asn	Val	Leu	Ala	Gly	Ile	Gly	Ile	Ala	Gln	Leu	Ala		
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gtt	ctg	gat	gac	cgg	gta	cat	gcc	aga	cgg	gcg	gtt	ttc	gag	cgc	tat	1301	
Val	Leu	Asp	Asp	Arg	Val	His	Ala	Arg	Arg	Ala	Val	Phe	Glu	Arg	Tyr		
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aag	gag	gcg	ctt	tcc	ggt	atc	gaa	ggt	ata	gaa	ttc	atg	cct	gag	gcc	1349	
Lys	Glu	Ala	Leu	Ser	Gly	Ile	Glu	Gly	Ile	Glu	Phe	Met	Pro	Glu	Ala		
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Gly	Met	Ser	Asn	Arg	Trp	Leu	Thr	Thr	Leu	Thr	Leu	Asp	Thr	Ala	Lys		
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Ile	Gln	Thr	Thr	Pro	Ala	Asp	Ile	Ile	Glu	Gln	Leu	Ala	Asn	Glu	Asn		
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att	gag	gcc	cgc	ccg	tta	tgg	aag	cct	ttg	cac	aga	cag	ccc	ctt	ttt	1493	
Ile	Glu	Ala	Arg	Pro	Leu	Trp	Lys	Pro	Leu	His	Arg	Gln	Pro	Leu	Phe		
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Lys	Gly	Ala	Ala	Phe	Tyr	Pro	His	Asp	Asp	Gln	Gly	Ser	Val	Cys	Cys		
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gac	tta	ttt	cag	cgc	ggg	ctc	tgc	ctg	ccg	tca	gga	tca	agt	atg	acg	1589	
Asp	Leu	Phe	Gln	Arg	Gly	Leu	Cys	Leu	Pro	Ser	Gly	Ser	Ser	Met	Thr		
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10295.204.ST25.txt

Arg Lys Glu Gln Asp Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys
 365 370 375

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 Tyr Lys
 380

agctggcaga aattttggat gtcattccaa ggcattcatc agtcgtttac ttggactacc 1753
 cgctatacgg aaacgtcggg gatctattga tcatgaaagg aacggaagct ttttttgaag 1813
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 tgccgcagtc gatttattat gagcatgaag aaaatataat aaaaacgcgc ggcatttttg 2053
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 agcgtttcga agaggtgaaa aacatcaaaa 2143

<210> 163
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 <212> PRT
 <213> Bacillus licheniformis

<400> 163

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 20 25 30

Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu Lys Leu Ala Ala Tyr
 35 40 45

Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser Gly Thr Ala Ala Ile
 50 55 60

His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys Gly Asp Thr Val Phe
 65 70 75 80

Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn Pro Ile Ile Tyr Glu
 85 90 95

Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg Asp Thr Trp Asn Met
 100 105 110

Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu Ala Glu Arg Ala Arg
 115 120 125

Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu Tyr Gly Gln Ser Ala
 130 135 140

Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg Phe Ala Val Pro Val
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10295.204.ST25.txt

145 150 155 160
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 165 170 175
 Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser Phe Asn Gly Asn Lys
 180 185 190
 Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val Ser Asp Asp Glu Asp
 195 200 205
 Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln Ala Arg Glu Pro Ala
 210 215 220
 Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn Tyr Arg Met Ser Asn
 225 230 235 240
 Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala Val Leu Asp Asp Arg
 245 250 255
 Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr Lys Glu Ala Leu Ser
 260 265 270
 Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala Gly Met Ser Asn Arg
 275 280 285
 Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys Ile Gln Thr Thr Pro
 290 295 300
 Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn Ile Glu Ala Arg Pro
 305 310 315 320
 Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe Lys Gly Ala Ala Phe
 325 330 335
 Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys Asp Leu Phe Gln Arg
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10295.204.ST25.txt

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aggcggggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat 180
tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaagt 240
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ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga 420
ataaaatcaa gccgtgccaa tttagcggca ggcatacataa cttatttttg aactttttga 480
atthagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt 533
Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe
1 5 10
caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac 581
Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp
15 20 25
agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga 629
Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg
30 35 40
ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga 677
Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly
45 50 55
acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg 725
Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly
60 65 70 75
gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc 773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Ala Thr Ala Glu Ala
80 85 90
gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa 821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu
95 100 105
aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct 869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala
110 115 120
act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg 917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met
125 130 135
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag 965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu
140 145 150 155
gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag ccg cct gtc ggc 1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly
160 165 170
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg 1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu
175 180 185
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca 1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala

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10295.204.ST25.txt

190 195 200

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205 210 215

ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc 1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala
220 225 230 235

gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa 1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln
240 245 250

aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag 1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu
255 260 265

cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat 1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His
270 275 280

ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg 1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu
285 290 295

aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat 1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His
300 305 310 315

ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct 1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro
320 325 330

ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct 1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro
335 340 345

ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa 1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys
350 355 360

aaa gga gga ggg gaa aag tgacgggttca ttttggttta atcggctgcg 1637
Lys Gly Gly Gly Glu Lys
365

gctatatgtc aagaaaacat cttcaagcac tggccgagtgc cgatgatgca aagttgtcgg 1697

ccgtcagtga tttgcaggaa gaaagaatga aggaagcggga agaatactat gcttccctcg 1757

ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgtgctt tcagatccta 1817

aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg 1877

cgctgctggc aggcaagcac gtcatcgtcg aaaaaccgat gaccttgtca ttacgggatg 1937

ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga 1997

tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa 2057

agatctactt gggcacggta tcgctccgct taaacaggtc ccccgcttat 2107

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<213> Bacillus licheniformis

10295.204.ST25.txt

<400> 165

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Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
 35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
 50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
 65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
 85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
 100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
 115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
 130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
 145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
 165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
 180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
 195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
 210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
 225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
 245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
 260 265 270

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Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
355 360 365

Lys

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15 20 25

aca aaa ggc cct tat gtc aga aca ttt gct gat cat atg aga cag tat 629
Thr Lys Gly Pro Tyr Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr
30 35 40

10295.204.ST25.txt

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gtc tca gac ttc tcg ttc ccc gcc act gtc aat gta ata gaa gat tta Val Ser Asp Phe Ser Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu 80 85 90	773
gga gcc aag ccg gtt ttt gcc gat gtt gat ctt gaa aca ttt aac atg Gly Ala Lys Pro Val Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met 95 100 105	821
ctt cca gaa gaa ctg gaa agt caa atc acg tcc cgt aca aaa gcc gtt Leu Pro Glu Glu Leu Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val 110 115 120	869
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caa att tgt aag gag tac ggc tta ccc ctt gtg gat gat gcc gct tgt Gln Ile Cys Lys Glu Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys 140 145 150 155	965
gcg atc ggc agc agc gaa tac ggc tgt aaa tcc gga aaa att gcc gat Ala Ile Gly Ser Ser Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp 160 165 170	1013
ctc acc tgt ttc agc ttt cac cca aga aag ctg ctt acg aca ggc gaa Leu Thr Cys Phe Ser Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu 175 180 185	1061
ggc ggg gca att aca acc gac cgg gaa gag ttg aaa gac tgg ctt tcg Gly Gly Ala Ile Thr Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser 190 195 200	1109
gtc aaa tta aac cat ggc gct gcc atc tct gac gga aaa ttg gat ttt Val Lys Leu Asn His Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe 205 210 215	1157
ata gat ttc ggc tac aac tac aga tta tcc gat atc caa gcc gct ctt Ile Asp Phe Gly Tyr Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu 220 225 230 235	1205
gga att aaa cag ctc caa aaa ctt gat gac atc att cat cgg aga aac Gly Ile Lys Gln Leu Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn 240 245 250	1253
ctt cag cag aaa gca tat agt gaa cag ctt gaa ccc ctc gga ttc caa Leu Gln Gln Lys Ala Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln 255 260 265	1301
agt caa aaa atc ggt cca gcc gtt gta cac aac ata caa tcc gcc gtt Ser Gln Lys Ile Gly Pro Ala Val Val His Asn Ile Gln Ser Ala Val 270 275 280	1349
ttc aaa gtt cca aaa aac atc gtt cgc gac gaa ttg att caa tat ttg Phe Lys Val Pro Lys Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu 285 290 295	1397
agc gac tgc cat ata gag tcg act ttc ggc act tat tgt tta agc ggc Ser Asp Cys His Ile Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly 300 305 310 315	1445

10295.204.ST25.txt

act ccc tat tac cgc cgg aaa tac caa cag cta aaa tcg aat tct ctc 1493
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 320 325 330

ttt ctt gaa caa cat acg att acc ctc cct tgc cat gat gaa gtc gat 1541
 Phe Leu Glu Gln His Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp
 335 340 345

tta gat cat gtg gtt tca gcc ata caa tca ttt atc aaa ttt aag gtt 1589
 Leu Asp His Val Val Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val
 350 355 360

gat tagttcaaaa tatcccggtc acagagaata gtgaacggga tattttttat 1642
 Asp

tcttaataca agaataaaaa aacaggtagt aaaccataga tttaccacct gattcattca 1702
 cataacaata cagcgaactt ccatgaaaaa aaacattcac ctgtagatta agagacagtt 1762
 ggaccgagaa tatatgcaaa tctgttagaa tgaaaatgct agtggaatat tcgatgtttt 1822
 tacaagcatc gtttaatat tggacagaca atgtgtaact ctcaattgta caattagttt 1882
 tcttttaaaga gaaactgctc cgcaagaaaa acctacggaa cagcttccta atgagaatat 1942
 taattagaaa gtttttcgat ttggatatga ccgctgtttc ctgtagcaag agttaacgct 2002
 aatccagtga cggcaatctg aatagtagaa gggacagcag taacttcaat catagcttct 2062
 cccactaatg gagtacctac gctgattaaa 2092

<210> 167
 <211> 364
 <212> PRT
 <213> Bacillus licheniformis

<400> 167

Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe Glu Glu Val Gln Ala
 1 5 10 15

Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu Thr Lys Gly Pro Tyr
 20 25 30

Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr Val Ser Ala Lys His
 35 40 45

Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu Ser Met Cys Leu Lys
 50 55 60

Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile Val Ser Asp Phe Ser
 65 70 75 80

Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu Gly Ala Lys Pro Val
 85 90 95

Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met Leu Pro Glu Glu Leu
 100 105 110

10295.204.ST25.txt

Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val Leu Phe Val Asp Ala
 115 120 125
 Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys Gln Ile Cys Lys Glu
 130 135 140
 Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys Ala Ile Gly Ser Ser
 145 150 155 160
 Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp Leu Thr Cys Phe Ser
 165 170 175
 Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu Gly Gly Ala Ile Thr
 180 185 190
 Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser Val Lys Leu Asn His
 195 200 205
 Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe Ile Asp Phe Gly Tyr
 210 215 220
 Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu Gly Ile Lys Gln Leu
 225 230 235 240
 Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn Leu Gln Gln Lys Ala
 245 250 255
 Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln Ser Gln Lys Ile Gly
 260 265 270
 Pro Ala Val Val His Asn Ile Gln Ser Ala Val Phe Lys Val Pro Lys
 275 280 285
 Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu Ser Asp Cys His Ile
 290 295 300
 Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly Thr Pro Tyr Tyr Arg
 305 310 315 320
 Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu Phe Leu Glu Gln His
 325 330 335
 Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp Leu Asp His Val Val
 340 345 350
 Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val Asp
 355 360

<210> 168
 <211> 1663
 <212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1163)

<400> 168

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ggcatttttc	cgtgcgccgt	cactcttgcc	tcgttggtg	gaaagccttt	tacagaggaa	180
atcacgagtc	tcttcatttc	gtccgcaagt	ctgggaggag	cgcttctttc	attcttgatc	240
ggctggggcg	ttgatgcaag	cgcagccgct	gtcttcccgt	ttttgctggt	cggcggattg	300
gggggcttgc	tgctggcgat	cagcgcggtg	atttttttat	ccggcctgca	aaaaaacaag	360
cagagtcatt	tgatatgta	gatttattag	gaagagatta	caagcttagt	aggatttttt	420
tcagcagccg	tttaaaccgt	tccatctttg	accataatat	tgctagaaaa	ggttgaagaa	480
cgagaggaac	ggtggggaaa	atg aag aaa tca aac att gcc tgt atg tat att				533
		Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile				
		1 5 10				
ttt ctt tta tta ata gga gcg ctt gca aat ctc acg acg gaa gag act						581
Phe Leu Leu Leu Ile Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr						
	15		20		25	
gcc caa tca tca ggc ggg cag cct gcc gtg att cct gat gaa gcg att						629
Ala Gln Ser Ser Gly Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile						
	30		35		40	
cgg ctg cgg att ttg gca aac agc gac agc ggg agc gac cag agc gtc						677
Arg Leu Arg Ile Leu Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val						
	45		50		55	
aaa cgc aaa atc agg gat gag gtc aat aaa caa att acg aaa tgg gtg						725
Lys Arg Lys Ile Arg Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val						
	60		65		70	75
gaa aac ctg acc tcg gtt gag gaa gcg aga caa gtc atc agg tcg aag						773
Glu Asn Leu Thr Ser Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys						
	80		85		90	
ctg cct gaa atc caa gag gtt gcc atg gat gtc atg aaa cgc gaa aat						821
Leu Pro Glu Ile Gln Glu Val Ala Met Asp Val Met Lys Arg Glu Asn						
	95		100		105	
gtt cgg caa tcc gtg tct gtc cgt ttt gat cgt gtt tca ttt ccg aca						869
Val Arg Gln Ser Val Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr						
	110		115		120	
aag cta tac ggc aat atg gtg tat ccg gcc gga gaa tat gag gct gtt						917
Lys Leu Tyr Gly Asn Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val						
	125		130		135	
tta att aca tta ggc aag gga gag gga gcc aac tgg tgg tgc gtc ctg						965
Leu Ile Thr Leu Gly Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu						
	140		145		150	155
ttt ccg cca ctt tgc ttt ctt gat ttt tcc aat ggg gaa gcc gta aag						1013
Phe Pro Pro Leu Cys Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys						
	160		165		170	

10295.204.ST25.txt

tcg cct gaa gac gaa caa acc gct gcc gga gaa gac cgc cgg gaa gaa 1061
 Ser Pro Glu Asp Glu Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu
 175 180 185

aaa aca gac gcg gcg gat gaa acg gta tct ggc ata gat aaa gat aaa 1109
 Lys Thr Asp Ala Ala Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys
 190 195 200

gaa gac aaa gaa gtg aaa ttt ttt ctt gtc gaa tgg att acc ggg ctt 1157
 Glu Asp Lys Glu Val Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu
 205 210 215

ttt tct taaaaggacc gccttgcttt cgtgtgcagg gcgggtttttt actgtttgtt 1213
 Phe Ser
 220

ttttcatgat ggttattgaa gcttttgaat atgatataat tttccaaaac ggttcagggg 1273

aaatactgct tttcggatat acaccttttg cccctttctg atgtgccaat cacattgccg 1333

gcagaagaga aactgtctta tcaccagtac agcgttcatt tgcataactca ttcaaagcgt 1393

tggttcctgc taatcaaaaat tgaaaaatga atagccggca ttcttccaaa tcaaaaggta 1453

tattttactg tcgccctcat agattggata gagaagttaa aaaacggggg gaaaagatgt 1513

tctaccaatt gaggttagcg gaaacgaaag acatgaatgc gatcgaagca tttttaaaaa 1573

aggcggggac aagccataag ggtcttgagg aagcgaagag ccagtttatc atgatggaag 1633

accctcccga tgaaatcgtc gcctgcctcg 1663

<210> 169

<211> 221

<212> PRT

<213> Bacillus licheniformis

<400> 169

Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile Phe Leu Leu Ile
 1 5 10 15

Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr Ala Gln Ser Ser Gly
 20 25 30

Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile Arg Leu Arg Ile Leu
 35 40 45

Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val Lys Arg Lys Ile Arg
 50 55 60

Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val Glu Asn Leu Thr Ser
 65 70 75 80

Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys Leu Pro Glu Ile Gln
 85 90 95

Glu Val Ala Met Asp Val Met Lys Arg Glu Asn Val Arg Gln Ser Val
 100 105 110

10295.204.ST25.txt

Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr Lys Leu Tyr Gly Asn
 115 120 125

Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val Leu Ile Thr Leu Gly
 130 135 140

Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu Phe Pro Pro Leu Cys
 145 150 155 160

Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys Ser Pro Glu Asp Glu
 165 170 175

Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu Lys Thr Asp Ala Ala
 180 185 190

Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys Glu Asp Lys Glu Val
 195 200 205

Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu Phe Ser
 210 215 220

<210> 170
 <211> 1351
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(851)

<400> 170
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 cggtcagcca atatgaaacg catccgatgt ataaacgtaa cgaaatcatt tccgatttga 120
 aggtcaataa aggccgtgag caaaaaataa accttgtcac atcagaaccg atttcccttt 180
 tgacgaaaaa aggcgaaaat atcgaatctg ttaaaaaaga aatcaaacag aaagaagata 240
 tccaggcccc tgtcaaaaaa ggcacagagc ttgggacgct cgttttgaaa aaggatggaa 300
 aggtgctcgc tgaaagtcct cttgtcgtcg aaaaagatat ggacaaagcg gggatgtgga 360
 cgatgtttcaa gcggacgatg acccactgga cgaagtggag tgaataatgc cgaacgggtca 420
 ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca ttatccgatt 480
 taaaccaagg aggaatgagg atg agc ctc gga atc gat att cac gtc aaa gaa 533
 Met Ser Leu Gly Ile Asp Ile His Val Lys Glu
 1 5 10
 tcc gta tta tgc att cgg ttg aca ggt gaa ctc gat cac cat aca gca 581
 Ser Val Leu Cys Ile Arg Leu Thr Gly Glu Leu Asp His His Thr Ala
 15 20 25
 gaa acc ttg aga aaa caa gtc agt gac cat ctg gaa caa acc gac att 629
 Glu Thr Leu Arg Lys Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile
 30 35 40
 cgc cat att gtc atg aat ctt gca gac ctt tcg ttt atg gac agt tca 677

10295.204.ST25.txt

Arg His Ile Val Met Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser
 45 50 55

ggg ctt ggc gtc gtg ctc ggc aga tat aag gag att aag cag ctc ggc 725
 Gly Leu Gly Val Val Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly 75
 60 65 70

gga gaa atg atc gtc tgc gcc att tcc cct gct gtc aaa cgt tta ttt 773
 Gly Glu Met Ile Val Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe 90
 80 85

gat atg tcc ggg ctg ttt aaa atc att cgc ctt gag caa tca gag cag 821
 Asp Met Ser Gly Leu Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln 105
 95 100

cgt gca ctt gaa acg ttg ggg gtg gcg tca tgaaaaatga aatgaacatt 871
 Arg Ala Leu Glu Thr Leu Gly Val Ala Ser 115
 110

cagtttacag cgctcagcca aaatgaatcg tttgcacggg tgacagtcgc tgctttttatc 931

gctcagcttg acccgacgat ggatgaactg accgaaatta aaacgggtcgt atccgaagcg 991

gtcacaacacg cgatcattca cggttatgaa aactcagggc agggaaacgt atatatttcc 1051

gtcactctcg aggaccatat tgtctatttta acgatccgcg acgaaggagt cggcatccct 1111

aatcttgaag aagcgcgcca gcccctgttc acgacaaagc ctgaactcga gcggtcggga 1171

atgggcttta cgatcatgga aaatttcatg gatgatattt cgatcgactc ctcacctgag 1231

atgggaacca caatacactt aacaaagcac ttatcaaaaa gcaaagcgct ttgcaattaa 1291

gggagatttg ttatggatgt ggaggttaaa aaagaaaacc agaacactca gcttaaagac 1351

<210> 171

<211> -117

<212> PRT

<213> Bacillus licheniformis

<400> 171

Met Ser Leu Gly Ile Asp Ile His Val Lys Glu Ser Val Leu Cys Ile
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Arg Leu Thr Gly Glu Leu Asp His His Thr Ala Glu Thr Leu Arg Lys
 20 25 30

Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile Arg His Ile Val Met
 35 40 45

Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser Gly Leu Gly Val Val
 50 55 60

Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly Gly Glu Met Ile Val
 65 70 75 80

Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe Asp Met Ser Gly Leu
 85 90 95

Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln Arg Ala Leu Glu Thr
 Page 246

10295.204.ST25.txt

100

105

110

Leu Gly Val Ala Ser
115

<210> 172
<211> 1438
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(938)

<400> 172
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cgaacggtca ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca 120
ttatccgatt taaaccaagg aggaatgagg atgagcctcg gaatcgatat tcacgtcaaa 180
gaatccgtat tatgcattcg gttgacaggt gaactcgatc accatacagc agaaaccttg 240
agaaaacaag tcagtgaacca tctggaacaa accgacattc gccatattgt catgaatctt 300
gcagaccttt cgtttatgga cagttcaggg cttggcgtcg tgctcggcag atataaggag 360
attaagcagc tcggcggaga aatgatcgtc tgcgccattt cccctgctgt caaacgttta 420
tttgatatgt ccgggctggt taaaatcatt cgccttgagc aatcagagca gcgtgcactt 480
gaaacgttgg ggggtggcgtc atg aaa aat gaa atg aac att cag ttt aca gcg 533
Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala
1 5 10
ctc agc caa aat gaa tcg ttt gca cgg gtg aca gtc gct gct ttt atc 581
Leu Ser Gln Asn Glu Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile
15 20 25
gct cag ctt gac ccg acg atg gat gaa ctg acc gaa att aaa acg gtc 629
Ala Gln Leu Asp Pro Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val
30 35 40
gta tcc gaa gcg gtc aca aac gcg atc att cac ggt tat gaa aac tca 677
Val Ser Glu Ala Val Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser
45 50 55
ggg cag gga aac gta tat att tcc gtc act ctc gag gac cat att gtc 725
Gly Gln Gly Asn Val Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val
60 65 70 75
tat tta acg atc cgc gac gaa gga gtc ggc atc cct aat ctt gaa gaa 773
Tyr Leu Thr Ile Arg Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu
80 85 90
gcg cgc cag ccc ctg ttc acg aca aag cct gaa ctc gag cgg tcg gga 821
Ala Arg Gln Pro Leu Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly
95 100 105
atg ggc ttt acg atc atg gaa aat ttc atg gat gat att tcg atc gac 869
Met Gly Phe Thr Ile Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp
110 115 120
tcc tca cct gag atg gga acc aca ata cac tta aca aag cac tta tca 917
Ser Ser Pro Glu Met Gly Thr Thr Ile His Leu Thr Lys His Leu Ser

10295.204.ST25.txt

125

130

135

aaa agc aaa gcg ctt tgc aat taagggagat ttgttatgga tgtggaggtt 968
 Lys Ser Lys Ala Leu Cys Asn
 140 145
 aaaaaagaaa accagaacac tcagcttaaa gaccatgaag tgaaagaact gattaaaaac 1028
 agccagaacg gcgatcaaaa agcaaggagc ctctcatag aaaaaaacat gcgtcttggt 1088
 tggctctgtcg tttagcgttt ttgaacaga ggctatgagc ctgacgacct ctttcaaact 1148
 ggctgcatcg gcctcttgaa gtcgggtggac aaattcgatc ttctctatga cgttcggttt 1208
 tccacctacg ccgttccgat gattatcggc gagattcagc ggtttatcag agatgacgga 1268
 accgtcaaag tgagccgctc gctgaaagaa ctggcaaca aaatccggcg ggcgaaagac 1328
 gagctttcca agtcaaacgg ccggattccg accgttcagg aaatcgccga ttatctcgaa 1388
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<210> 173
 <211> 146
 <212> PRT
 <213> Bacillus licheniformis

<400> 173

Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala Leu Ser Gln Asn Glu
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Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile Ala Gln Leu Asp Pro
20 25 30

Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val Val Ser Glu Ala Val
35 40 45

Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser Gly Gln Gly Asn Val
50 55 60

Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val Tyr Leu Thr Ile Arg
65 70 75 80

Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu Ala Arg Gln Pro Leu
85 90 95

Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly Met Gly Phe Thr Ile
100 105 110

Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp Ser Ser Pro Glu Met
115 120 125

Gly Thr Thr Ile His Leu Thr Lys His Leu Ser Lys Ser Lys Ala Leu
130 135 140

Cys Asn
145

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<210> 174
<211> 5482
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501)..(4982)
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[illegible]

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ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile 175 180 185	1061
gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro 190 195 200	1109
agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg 205 210 215	1157
atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala 220 225 230 235	1205
cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro 240 245 250	1253
ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro 255 260 265	1301
cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu 270 275 280	1349
att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys 285 290 295	1397
aga gaa gaa aaa aga gag cgg gtc tat acc ctt tac ctt gaa aac aaa Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys 300 305 310 315	1445
aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp 320 325 330	1493
ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile 335 340 345	1541
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln 350 355 360	1589
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu 365 370 375	1637
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln 380 385 390 395	1685
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile 400 405 410	1733
act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser 415 420 425	1781

10295.204.ST25.txt

gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe 430 440	1829
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu 445 450 455	1877
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro 460 465 470 475	1925
cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln 480 485 490	1973
ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu 495 500 505	2021
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr 510 515 520	2069
aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly 525 530 535	2117
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys 540 545 550 555	2165
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu 560 565 570	2213
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro 575 580 585	2261
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc cgg Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg 590 595 600	2309
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro 605 610 615	2357
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp 620 625 630 635	2405
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu 640 645 650	2453
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn 655 660 665	2501
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr 670 675 680	2549
ggg tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597

10295.204.ST25.txt

gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa 2645
Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys
700 705 710 715

ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga 2693
Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly
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735 740 745

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Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln
750 755 760

tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa 2837
Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys
765 770 775

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845 850 855

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Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val
895 900 905

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gcc acg acg ttc atg atg agc ttt gcc gaa cag tat acg ccg gaa Ala Thr Thr Phe Met Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu 1020 1025 1030	3599
gaa ttg cat tac tac att ttc gac ttt ggc aac gga acg ctg ctt Glu Leu His Tyr Tyr Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu 1035 1040 1045	3644
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gca gaa cgc tcg gaa ggc atg Ala Glu Arg Ser Glu Gly Met 1230 1235	aga aag ccg gcg cct Arg Lys Pro Ala Pro 1240	gtg ccg atg Val Pro Met	4229
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gtc aga cac gcg atg cta ttg Val Arg His Ala Met Leu Leu 1440 1445	atg aaa aaa tcc gag Met Lys Lys Ser Glu 1450	cag aac ttg Gln Asn Leu	4859
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 tgtcaaacag 5482

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 <212> PRT
 <213> Bacillus licheniformis

<400> 175

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Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile Gly Pro Asp Leu Lys
 20 25 30

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
 35 40 45

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
 50 55 60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
 65 70 75 80

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
 85 90 95

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
 100 105 110

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
 115 120 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
 130 135 140

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala

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425

420

430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
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Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
515 520 525

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
530 535 540

Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
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His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
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Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
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690

695

700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
 705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
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Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
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Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
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Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
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Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
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Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
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Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
 820 825 830

Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
 835 840 845

Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
 850 855 860

Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
 865 870 875 880

Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
 885 890 895

Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
 900 905 910

Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
 915 920 925

Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
 930 935 940

Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
 945 950 955 960

Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
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970

965

975

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980 985 990

Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
995 1000 1005

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Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
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Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
1070 1075 1080

Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
1085 1090 1095

Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
1100 1105 1110

Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
1115 1120 1125

Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
1130 1135 1140

Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
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Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
1160 1165 1170

Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
1175 1180 1185

Ile Pro Gly Arg Val Ile Ile Asn Lys Glu Asn Gln Tyr Phe Ala
1190 1195 1200

Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
1205 1210 1215

Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu
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1220

1225

1230

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Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
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 1310 1315 1320

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 1325 1330 1335

Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
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Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
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Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
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Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
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Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
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Leu Leu Met Lys Lys Ser Glu Gln Asn Leu Ile Gln Leu Pro Tyr
 1445 1450 1455

Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly Phe Gly Tyr Ile Val
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Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile Pro Leu Cys Ala Val
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1485

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agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa Ser Asp Asp Leu Ala Leu Ala Leu Ala Lys Asp Ile Arg Ile Glu 380 385 390 395			1685
gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 1733			

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att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu 700 705 710 715			2645
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val 720 725 730			2693
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745			2741
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly 750 755 760			2789
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu 765 770 775			2837
tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac Ser Ser 780			2893
atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat			2953
ctgatctgtc agacggaggg aaaacatgtc gataaaagct gacatcaacg gttatgttta			3013
aagggtgattg atcggataaa agatgatatt caaaatgggg tcttttgcca aaatgaacgg			3073
ctcccgagtg aatttgagct gtcaaagatg cttggtgtga gcagaacggc tttgcgtgag			3133
gcgcttagaa tactggaaga agaaaacgtc atcatcagaa ggcatggagt cggacatttt			3193
gtaaatgccca gaccgttatt tctatcaggt attgagcagc tgaacagcgt cacaaaaatg			3253
atcgagcagg caagcatgac gccgggaacc atttttatgt cctcacaggt taccgctccc			3313
actgaagaag atatgctccg gtttcaatat			3343

<210> 177
 <211> 781
 <212> PRT
 <213> Bacillus licheniformis

<400> 177

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys
 1 5 10 15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala
 20 25 30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe
 35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
 50 55 60

10295.204.ST25.txt

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
 65 70 75 80
 Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
 85 90 95
 Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
 100 105 110
 Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
 115 120 125
 Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
 130 135 140
 Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
 145 150 155 160
 Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
 165 170 175
 Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
 180 185 190
 Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
 195 200 205
 Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
 210 215 220
 Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
 225 230 235 240
 Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
 245 250 255
 Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
 260 265 270
 Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
 275 280 285
 Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
 290 295 300
 Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
 305 310 315 320
 His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
 325 330 335

10295.204.ST25.txt

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
 340 345 350
 Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
 355 360 365
 Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
 370 375 380
 Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
 385 390 395 400
 Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
 405 410 415
 Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
 420 425 430
 Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
 435 440 445
 Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
 450 455 460
 Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
 465 470 475 480
 Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
 485 490 495
 Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
 500 505 510
 Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
 515 520 525
 Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
 530 535 540
 Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
 545 550 555 560
 Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
 565 570 575
 Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
 580 585 590
 Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
 595 600 605

10295.204.ST25.txt

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780

<210> 178
<211> 1735
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1235)

<400> 178
gatattgtgc gtaaacta tcttccgac cggtgaagac gagttcgacg tcgggattct 60
gttttgcaaa ctgctcaaac cgttgtttta ttgcagtctg gccttttctt ttgtacgctt 120
tttgatcaat ccattcgctg aaatacgcaa tggaagtctc cttgctgccg atatcttgct 180
gaataatgtc gttcagttca tcgatattgt ctttcgcact tctcaaaatc tcatcctcga 240
gcgtgctgct ggccgtaaaa tatgaagtaa ccgaaagaac caagatcgga attgttaaaa 300
tgaatataaa tgagaaaatt aatttttttag aaatagaagg acgtttcgtc caatttaaaa 360

10295.204.ST25.txt

gctttttcat gtgtgattcc cttttctcta cttttatcgg agacggggtc ttttttttaa 420
ataaaaaaag cggaaaatta gaccgttttc ctgccaagc atcaggcata cgctaataaa 480
aaaggaaaag ggtgtatcct atg ata agt gtt tgc ggc tac cgg ctc cgt cct 533
Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro
1 5 10
gag gat atc gaa aaa ctg aat gtc agt cag acg cag aga gac atc gca 581
Glu Asp Ile Glu Lys Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala
15 20 25
aac cgg atg ctg gcc atg ccg tcc gga tat aga tac ggt tca atc tca 629
Asn Arg Met Leu Ala Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser
30 35 40
gaa ctg tta ttt gag ctg aga ttc aga gag cat acc gtc aaa tgc gcc 677
Glu Leu Leu Phe Glu Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala
45 50 55
aga gag ctg atc aac agc gga gcg aag ttt gcc acc ttt tca aag aca 725
Arg Glu Leu Ile Asn Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr
60 65 70 75
tac ggg aat gaa gag ttt tgg agg gtg acg cct gag ggg gct ttg gag 773
Tyr Gly Asn Glu Glu Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu
80 85 90
ttg aag tac agg gca ccg gct tca aag gcg att cga aat att ttt gaa 821
Leu Lys Tyr Arg Ala Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu
95 100 105
agc ggc cct tct tat gct ttt gag tgc gcg act gcg att gtc atc att 869
Ser Gly Pro Ser Tyr Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile
110 115 120
ttt tat atg gcg ctt ctc aaa acg atc ggc gac cag aca ttt gac cgg 917
Phe Tyr Met Ala Leu Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg
125 130 135
aat tat caa agg atc att tta tac gat tgg cac tat gag cgg ctg ccg 965
Asn Tyr Gln Arg Ile Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro
140 145 150 155
atc tat acg gat aaa gga aac gac tac ctt ccg gga gac tgc ctg tat 1013
Ile Tyr Thr Asp Lys Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr
160 165 170
ttc aag aac cct gaa ttc gat ccc tca aga ccg cag tgg cgc gga gaa 1061
Phe Lys Asn Pro Glu Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu
175 180 185
aat gct att tta ctt gaa aat aat ctc tat gcg gca cac ggc ctg ggg 1109
Asn Ala Ile Leu Leu Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly
190 195 200
atc tta agc ggc gaa aca atc att gaa aaa ctg aac ggg ctg aga aag 1157
Ile Leu Ser Gly Glu Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys
205 210 215
cct cat gca cag acg tcc gcc tat ctg ctt tcc caa gtg acg cgg gtt 1205
Pro His Ala Gln Thr Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val
220 225 230 235
gat att ccg gca tta att caa atg atc aga tagcacatcg gccggcacia 1255
Asp Ile Pro Ala Leu Ile Gln Met Ile Arg
240 245

10295.204.ST25.txt

gctgatccat cagctccttc accgtcgttt gctcgacggg ggcccgcacg ctctgtccgg 1315
 cccacaatga catgttatcc gtattcccgt caagcttcgc ctgttttctc atcggttgcg 1375
 tcagcgtggt ttgcagagga taaggcagcg cttcagcttc ttcttggcgt ctgtcttcca 1435
 tccactgatt gacgatgcct cttgccggct tccccgagaa caaacggggtc aggcttggtg 1495
 cggtttcaac cgcttcgaac aatttttgtt tgtaggcagg gtgtgttccg ctttcttcgc 1555
 acgtcaaaaa agcgggtaccg atttgaacgc cctgtgcgcc gagggcaaaa gctgcagcaa 1615
 cacctctttt gtcaaaaatg ccgcccgtg cgataactgg aaccgacaca tgatctgccg 1675
 cttggggaat taaagccatc gagccgacag caggctctcc cttcgttttc aagaaggctc 1735

<210> 179
 <211> 245
 <212> PRT
 <213> Bacillus licheniformis

<400> 179

Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro Glu Asp Ile Glu Lys
 1 5 10 15

Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala Asn Arg Met Leu Ala
 20 25 30

Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser Glu Leu Leu Phe Glu
 35 40 45

Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala Arg Glu Leu Ile Asn
 50 55 60

Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr Tyr Gly Asn Glu Glu
 65 70 75 80

Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu Leu Lys Tyr Arg Ala
 85 90 95

Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu Ser Gly Pro Ser Tyr
 100 105 110

Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile Phe Tyr Met Ala Leu
 115 120 125

Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg Asn Tyr Gln Arg Ile
 130 135 140

Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro Ile Tyr Thr Asp Lys
 145 150 155 160

Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr Phe Lys Asn Pro Glu
 165 170 175

10295.204.ST25.txt

Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu Asn Ala Ile Leu Leu
 180 185 190

Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly Ile Leu Ser Gly Glu
 195 200 205

Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys Pro His Ala Gln Thr
 210 215 220

Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val Asp Ile Pro Ala Leu
 225 230 235 240

Ile Gln Met Ile Arg
 245

<210> 180
 <211> 1405
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(905)

<400> 180
 aggctatact acagtctgag gtgattgaaa ttggccaaac gaaaagcaaa tcatgtaata 60
 aatggaatga acaatgcgaa acgccaagga aacggcgcg gatatatattga aaatgatcag 120
 cacatactca ctgaggcgga acgccaaaac aacaaaaaac ggaaaaccaa tcaataaata 180
 cgaaagatcc ttcattgaata tcttaggagg ttaaaacatt gacaaataaa aacgacggca 240
 aagatatgag caaaaacgca ccgaaaggag ctccagccggg gcagccagag cctttgagcg 300
 gaagcaaaaa agtaaaaaac cggaaccata caagacaaaa acacaattcc agtcacgata 360
 tgtaacattt tttccgcgcc tttcacggcg cggttttttt ccttaccgag cgtcacccctg 420
 aggcgttgat caccctcctt cacatgaatt caaagggtgtg cataatctaa tggttaaggct 480
 aggtatggag gaatgctcca atg aca aat aca aaa cgt ttc gat tcc gca gat 533
 Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp
 1 5 10
 ttt gat aaa gaa tgg atg aaa cag ttt gtt gac gac cct ttt ctc ctc 581
 Phe Asp Lys Glu Trp Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu
 15 20 25
 tat gat gaa act tta ccg att gac ctt tat gaa acg agc act gaa tat 629
 Tyr Asp Glu Thr Leu Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr
 30 35 40
 ata att gaa gca gat tta agc cac ttg aat gtc cgg cat ctt gac ttg 677
 Ile Ile Glu Ala Asp Leu Ser His Leu Asn Val Arg His Leu Asp Leu
 45 50 55
 acg ttt tca ggc tac gat ttc aag ctt gca gtt aaa acc gat gag cag 725
 Thr Phe Ser Gly Tyr Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln
 60 65 70 75

10295.204.ST25.txt

ctt tac gag aaa tcg ctg atg ctt cct ttc ttt ttg aat gac aaa cag 773
 Leu Tyr Glu Lys Ser Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln
 80 85 90
 atc gaa gcg gaa tgc gaa aac aac att ctt gca gtt aaa atc aat aaa 821
 Ile Glu Ala Glu Cys Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys
 95 100 105
 gaa tca agc aaa gat gac att tcg ctt tca atc aat att cct ttt ata 869
 Glu Ser Ser Lys Asp Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile
 110 115 120
 tca aac ctg cac aac aag cag aac ccg gac agc gct taaaacactt 915
 Ser Asn Leu His Asn Lys Gln Asn Pro Asp Ser Ala
 125 130 135
 gccatccggg tttttttccg ttcgttcgtc aaatatcctc tagcaattct ctatggccga 975
 ttagggaatc gctatacaat agattatggt ctagcatctc ttttgaccag gccggtgtcc 1035
 cattttatat tattttttct atgttcttct aaaacgcctt catgtaaaat aggttataga 1095
 caaaggagtg atgagagatg ctggaaggat ggtttttatg gctgatgctc gcttggatcg 1155
 tcatcatgat cgtcctcttg tcaatcggcg gttttttcat gtttcgcaaa tttttaaaaa 1215
 ggctgcctaa agaagatggg aaatctgagc tggactggca ggattattat attgaacaga 1275
 caaggcattt gtggaatgac gaagaaaaag aactgcttga ggaattgggt tcacccgtac 1335
 ccgagctgtt tcgcatgta gcaaaagcaa aaatcgccgg taagatcggg gagcttgcac 1395
 tgaaagaaaa 1405

<210> 181
 <211> 135
 <212> PRT
 <213> Bacillus licheniformis
 <400> 181

Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp Phe Asp Lys Glu Trp
 1 5 10 15

Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu Tyr Asp Glu Thr Leu
 20 25 30

Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr Ile Ile Glu Ala Asp
 35 40 45

Leu Ser His Leu Asn Val Arg His Leu Asp Leu Thr Phe Ser Gly Tyr
 50 55 60

Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln Leu Tyr Glu Lys Ser
 65 70 75 80

Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln Ile Glu Ala Glu Cys
 85 90 95

Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys Glu Ser Ser Lys Asp
 100 105 110

10295.204.ST25.txt

Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile Ser Asn Leu His Asn
 115 120 125

Lys Gln Asn Pro Asp Ser Ala
 130 135

<210> 182
 <211> 2155
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1655)

<400> 182
 aaagggttttc agaaagcttc ggcggtttctt ttgatgagct gatgacagcg gccggctatg 60
 cgatggagaa gacgcaggaa agcgaacgtc cggatattca ctcgtcagtt gccgaaattg 120
 aagatgtttt gcaaacctca aatgtctatg atcggccatt taccatggaa gaactgaaaa 180
 acaaattgaa tgagtgcgaa caatattctc agacggagga aggaaagcgt accattctgg 240
 ctgagtttga atctaaaatc gagaaagtgt cgggcattgg tccttttctg acccgtctgc 300
 acgacatgta cagcagattt acctcggggc gggggacgcc gcgtgaattg ctgctgatgg 360
 gcggcgcttt gctgtatttc atcgtttctg ttgatgtcat accggattat atttttccga 420
 tcggctatat cgatgatgcg gcagcggttc atttcgtttt caaccagctg tcatataaat 480
 catgatggag catgttcaag atg aaa aga aag cat atc aac att gac atc agt 533
 Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser 10
 1
 5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 100
 105
 110
 115
 120

10295.204.ST25.txt

ata ctc aat caa ttt cag cat aaa agg ttc tcc ttc gcc gag agc atc Ile Leu Asn Gln Phe Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile 125 130 135	917
att ccg acg gga aaa atc atg atg tac acg gtg att ccg ttt ttc ttt Ile Pro Thr Gly Lys Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe 140 145 150 155	965
ata ttg gtt cag cca gat tta ggg tcc gca ttg gtg att tta tcg atc Ile Leu Val Gln Pro Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile 160 165 170	1013
gca ttc acg ttg atg ctg gtc tcg ggg att tcg ggc agg atg atc gtg Ala Phe Thr Leu Met Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val 175 180 185	1061
tcc ctg tca ctt gga ttc atg gca ttg gtt gcc ttt ttg acg tat ttg Ser Leu Ser Leu Gly Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu 190 195 200	1109
cac aat cat tac ttt gag ata ttt tca aag att att aag cct cac cag His Asn His Tyr Phe Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln 205 210 215	1157
ctt gac cgg ata tat ggc tgg ctc agt cct cat gaa cat gcc tct aca Leu Asp Arg Ile Tyr Gly Trp Leu Ser Pro His Glu His Ala Ser Thr 220 225 230 235	1205
tat gga tac cag ctg acg cag gcg tta ttg ggg atc gga tca ggc cag Tyr Gly Tyr Gln Leu Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln 240 245 250	1253
ctg tca ggg agc ggc ttt act caa gga atc caa gtt cag gga ggg aaa Leu Ser Gly Ser Gly Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys 255 260 265	1301
att ccg gag gct cat act gat ttt att ttc gcc gtg att ggt gag gaa Ile Pro Glu Ala His Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu 270 275 280	1349
ttc ggt ttt ttg ggt gcc gta aca tta gtc tgt ctg tat ttt ctg atg Phe Gly Phe Leu Gly Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met 285 290 295	1397
atc tac aga atc atc agg att gcg ctt tcg tcc aac agt ctg ttc ggt Ile Tyr Arg Ile Ile Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly 300 305 310 315	1445
ctt tat ata tgt gcg ggg gtt gca ggg ttg att gta ttc caa gtg ttc Leu Tyr Ile Cys Ala Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe 320 325 330	1493
caa aat atc ggg atg acg atc ggg tta atg ccg atc acg ggg ctc gct Gln Asn Ile Gly Met Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala 335 340 345	1541
ctt ccg ttt atc agc tat ggc ggc agc gcg ctg ttg acc aac atg atc Leu Pro Phe Ile Ser Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile 350 355 360	1589
gct tta ggt ctc gtt ttc agt gtg aat atc aga tct aaa cat tac atg Ala Leu Gly Leu Val Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met 365 370 375	1637
ttt ggg aat gat tgg gga tgaagttgct caaaatgatt ctttcccatc Phe Gly Asn Asp Trp Gly 380 385	1685

10295.204.ST25.txt

taaagaaaact tgattatgta ttgattgccg cggttctgtt tttatctgcg tttggcttgc 1745
 tgatggtata cagcgccggc taccctctcg gatatatgaa gtatcatgat ggcagctatt 1805
 tttttatgaa gcagctgcaa tggctgctca tcggtttggc ctttttttcg gctgccgcc 1865
 ttttcccata caaagcttac agcaaactca ttcggttttt ggtgaagctt tcttttttaa 1925
 tgctgattct cgttttgctg ccgggaatcg ggatggagaa aaacaattcc caaaggtgga 1985
 ttcaattcgg ttcgctcatg attcagccgt ctgaggctgt gaagcttggt atggttattt 2045
 atttcgccta tgtgtatgca aaaaagcaga aatacatcgc cgatttcgga aagggcgtca 2105
 tgccgccgct gctgattttg gcggctgtgt tttttttgat tttaaaacag 2155

<210> 183

<211> 385

<212> PRT

<213> Bacillus licheniformis

<400> 183

Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser Leu Leu Leu Ile Leu
 1 5 10 15

Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val Tyr Ser Gly Ser Gly
 20 25 30

Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala Lys Arg Gln Val Phe
 35 40 45

Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly Thr Ala Tyr Ile Asp
 50 55 60

Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu Phe Val Gly Ala Val
 65 70 75 80

Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr Tyr Lys Asn Gly Ser
 85 90 95

Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile Gln Pro Ser Glu Phe
 100 105 110

Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser Ile Leu Asn Gln Phe
 115 120 125

Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile Ile Pro Thr Gly Lys
 130 135 140

Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe Ile Leu Val Gln Pro
 145 150 155 160

Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile Ala Phe Thr Leu Met
 165 170 175

10295.204.ST25.txt

Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val Ser Leu Ser Leu Gly
 180 185 190

Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu His Asn His Tyr Phe
 195 200 205

Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln Leu Asp Arg Ile Tyr
 210 215 220

Gly Trp Leu Ser Pro His Glu His Ala Ser Thr Tyr Gly Tyr Gln Leu
 225 230 235 240

Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln Leu Ser Gly Ser Gly
 245 250 255

Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys Ile Pro Glu Ala His
 260 265 270

Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu Phe Gly Phe Leu Gly
 275 280 285

Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met Ile Tyr Arg Ile Ile
 290 295 300

Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly Leu Tyr Ile Cys Ala
 305 310 315 320

Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe Gln Asn Ile Gly Met
 325 330 335

Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala Leu Pro Phe Ile Ser
 340 345 350

Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile Ala Leu Gly Leu Val
 355 360 365

Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met Phe Gly Asn Asp Trp
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Gly
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10295.204.ST25.txt

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 gacgaaaaaaa gcgctgtccg cctttcaaaa gccgggtcatt ttgctggcag gggggcttga 180
 ccgcggaaat gaatttgatg aactaaagcc gcatatgtct tttgtaaaag cgggtgatcac 240
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 acgtggtgac atgtttgtaa acgccgtgca tatgcttaaa taagggttg tctcgtaaag 480
 atagccctaa gaattagagc ttg ggg tgt tcg gct ttg caa aca aaa aaa acg 533
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 1 5 10
 tca ccg gat ttt ttg ctg gtt atc att acg cta ttg ctt tta aca atc 581
 Ser Pro Asp Phe Leu Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile
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 gga ctg att atg gta tac agc gcc agt gca gta tgg gcg act tac aaa 629
 Gly Leu Ile Met Val Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys
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 tac gac gac tcc ttt ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc 677
 Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly
 45 50 55
 atc ggg gtc atc gcc atg ttt ttc atc atg aac gtc gac tac tgg acg 725
 Ile Gly Val Ile Ala Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr
 60 65 70 75
 tgg agg act tat gcg aaa ata ctg atc att gta tgt ttc ttt ctg ctc 773
 Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu
 80 85 90
 atc atc gtc ctg gtt ccc ggg atc ggc atg gaa cgg aac ggg tcg agg 821
 Ile Ile Val Leu Val Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg
 95 100 105
 agc tgg atc gga gtc ggc gct ttc agc att cag ccg tcc gag ttt atg 869
 Ser Trp Ile Gly Val Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met
 110 115 120
 aaa ctc gcg atg atc gca ttt ttg gcc aag ttt tta tct gaa aag caa 917
 Lys Leu Ala Met Ile Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln
 125 130 135
 aag aat att acg tcg ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att 965
 Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile
 140 145 150 155
 gtc ttt tca gct ttt ctg atc atc atg atg cag cct gac ctc gga aca 1013
 Val Phe Ser Ala Phe Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr
 160 165 170
 gga acc gtg atg gtc ggc aca tgc atc att atg atc ttt gtc gcg ggg 1061
 Gly Thr Val Met Val Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly
 175 180 185
 gcg aga att tcg cac ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt 1109
 Ala Arg Ile Ser His Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly
 190 195 200

10295.204.ST25.txt

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att cag tct ctt tat gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly 240 245 250	1253
ctc ggc cag agc agg caa aag ttt ttc tat ctg cct gag ccg cag aca Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr 255 260 265	1301
gat ttt att ttt gcg att tta tca gag gag ctc ggc ttt atc ggc gga Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly 270 275 280	1349
tcg ctg att ctt ttg ctc ttc agc gtt cta tta tgg aga ggc atc aga Ser Leu Ile Leu Leu Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg 285 290 295	1397
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gtc att tcg atg ata gcg att cag gtt atg atc aat atc gga gtc gtg Val Ile Ser Met Ile Ala Ile Gln Val Met Ile Asn Ile Gly Val Val 320 325 330	1493
act ggt ttg att cct gtt aca ggc att acg ctt ccg ttt tta agc tat Thr Gly Leu Ile Pro Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr 335 340 345	1541
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 <400> 185

10295.204.ST25.txt

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 Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
 35 40 45
 Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
 50 55 60
 Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
 65 70 75 80
 Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
 85 90 95
 Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
 100 105 110
 Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
 115 120 125
 Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
 130 135 140
 Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
 145 150 155 160
 Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
 165 170 175
 Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
 180 185 190
 Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
 195 200 205
 Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
 210 215 220
 Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
 225 230 235 240
 Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
 245 250 255
 Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
 260 265 270

10295.204.ST25.txt

Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
 275 280 285

Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
 290 295 300

Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
 305 310 315 320

Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
 325 330 335

Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
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Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
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Ser Arg Tyr
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 cggcgttttc ggtaaagtac acagtgaatg acaaacagga acctgttttt ctcgaataga 300
 atatcgggtca aaatgcaagt atcagtcatg aacctttctc ctccggcatac aatgaggaga 360
 aagggtttttt catgtatgcc gaaaaaatTT ccctaagctg tcatattgaa ataggacaac 420
 gtcatacact atagtgtcct gtttttgatt gatgaagaag taaaaaattg aaaaggattg 480
 gaagtccggg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct 533
 Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala
 1 5 10
 gaa cga aca gga ggc gat ata tac tta ggt gtc gta gga gct gta cgt 581
 Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg
 15 20 25
 aca gga aaa tct acg ttt atc aaa aaa ttt atg gag cta gtg gtg ctc 629
 Thr Gly Lys Ser Thr Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu
 30 35 40
 ccg aat atc aac aat gaa gca gac cgg gcg cgc gca caa gat gag ctc 677
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10295.204.ST25.txt

Pro Asn Ile Asn Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu
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ccc caa agt gcc gct ggc aaa acc att atg aca act gaa ccg aag ttt 725
 Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe
 60 65 70 75

gtt ccg aat cag gca atg tca gtt cat gtc agt gac gga ctc gat gtg 773
 Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val
 80 85 90

aat ata agg ctt gtc gac tgc gtc ggc tat act gta ccc ggg gca aag 821
 Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys
 95 100 105

gga tac gag gat gaa aac ggg ccg aga atg atc aat act cct tgg tat 869
 Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr
 110 115 120

gaa gag ccg att ccg ttt cac gaa gct gcc gaa atc ggc acg aga aaa 917
 Glu Glu Pro Ile Pro Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys
 125 130 135

gtc atc caa gag cac tcc aca atc ggt gtt gtg att acg act gac ggc 965
 Val Ile Gln Glu His Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly
 140 145 150 155

acg att gga gaa atc gcc aga cag gat tat gtc gag gct gaa gaa cgg 1013
 Thr Ile Gly Glu Ile Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg
 160 165 170

gtg atc gac gag ttg aaa gag gtt gga aaa ccg ttt atc atg gtc atc 1061
 Val Ile Asp Glu Leu Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile
 175 180 185

aat tcc gta agg ccg tat cat ccg gaa aca gaa gcg ctc agg caa gaa 1109
 Asn Ser Val Arg Pro Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu
 190 195 200

ttg atg gaa aag tac gac att ccg gtg ctg gcg atg agc gtt gaa agc 1157
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 205 210 215

atg agg gaa gcg gac gtt ctg agc gtt ctc aga gaa gcg ctt tac gaa 1205
 Met Arg Glu Ala Asp Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu
 220 225 230 235

ttc cct gtg ctc gaa gtc aac gtc aat ctt cca agc tgg gtg atg gta 1253
 Phe Pro Val Leu Glu Val Asn Val Asn Leu Pro Ser Trp Val Met Val
 240 245 250

tta aaa gag aat cat tgg ctc agg gaa aac tat caa gat tcc gtt aaa 1301
 Leu Lys Glu Asn His Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys
 255 260 265

gaa acc gtc aaa gat att aaa aga ctg aga gat gtc gac cgc gtc gtc 1349
 Glu Thr Val Lys Asp Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val
 270 275 280

gga cac ttc agc gaa ttt gat ttc atc gag gcg gca agc ctc gcc gga 1397
 Gly His Phe Ser Glu Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly
 285 290 295

att gaa atg ggc cag ggg atc gcg gaa atc gat tta tac gcg ccg gat 1445
 Ile Glu Met Gly Gln Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp
 300 305 310 315

tac ctg tac gat gaa att ttg agg gaa gtc gtc ggc gtt gaa atc aga 1493

10295.204.ST25.txt

Tyr Leu Tyr Asp Glu Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg
 320 325 330
 gga aaa gat cac ctc ctt cag ctc atg cag gat ttt gcc cat gcc aag 1541
 Gly Lys Asp His Leu Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys
 335 340 345
 acc gaa tat gat caa gtc tca gat gca ttg aaa atg gtg aaa caa acc 1589
 Thr Glu Tyr Asp Gln Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr
 350 355 360
 ggc tat gga atc gca gct ccc gca tta acc gat atg agc ctg gat gaa 1637
 Gly Tyr Gly Ile Ala Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu
 365 370 375
 ccg gaa atc atc agg cag ggt tca aga ttc gga gtc cgg ctg aag gcg 1685
 Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala
 380 385 390 395
 gtg gcg ccg tcg att cat atg atc aaa gtc gat gtg gaa agc gag ttt 1733
 Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe
 400 405 410
 gcg ccg atc atc gga aca gag aag cag agc gaa gag ctt gtc cgc tat 1781
 Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr
 415 420 425
 tta atg cag gac ttt gag gac gat ccg ctg tca atc tgg aat tcc gac 1829
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 430 435 440
 ata ttc gga aga agc ttg agc tcg atc gtc aga gaa ggg att cag gcg 1877
 Ile Phe Gly Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala
 445 450 455
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 Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr
 460 465 470 475
 ctg gag cgc att atc aat gaa ggc tca ggc ggc ttg att gcg atc atc 1973
 Leu Glu Arg Ile Ile Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile
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Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg Thr Gly Lys Ser Thr
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Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Asn Asn
 35 40 45

10295.204.ST25.txt

Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala
 50 55 60

Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala
 65 70 75 80

Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val
 85 90 95

Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu
 100 105 110

Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro
 115 120 125

Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His
 130 135 140

Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Glu Ile
 145 150 155 160

Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg Val Ile Asp Glu Leu
 165 170 175

Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro
 180 185 190

Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu Leu Met Glu Lys Tyr
 195 200 205

Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ala Asp
 210 215 220

Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu
 225 230 235 240

Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His
 245 250 255

Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys Glu Thr Val Lys Asp
 260 265 270

Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly His Phe Ser Glu
 275 280 285

Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly Ile Glu Met Gly Gln
 290 295 300

Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp Tyr Leu Tyr Asp Glu
 305 310 315 320

10295.204.ST25.txt

Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg Gly Lys Asp His Leu
325 330 335

Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln
340 345 350

Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala
355 360 365

Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg
370 375 380

Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile
385 390 395 400

His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly
405 410 415

Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe
420 425 430

Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser
435 440 445

Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met
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485 490

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gacgcggcgc caataaagaa gcgcttgaga cggcccgtaa gctggaaaac aatgcacaga 180
tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg 240
atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag 300
cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg 360

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10295.204.ST25.txt

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cg	gg	at	tt	at	at	gt	tc	ct	gc	at	tt	at	at	ac	ct	1349
Arg	Gly	Ile	Phe	Ile	Ile	Val	Ser	Leu	Ala	Met	Phe	Met	Met	Thr	Leu	
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Ile	Thr	Ser	Thr	Val	Gln	Tyr	Phe	Arg	Asp	Lys	Asn	Gln	Arg	Lys	Lys	
	285					290					295					
aga	gaa	gaa	aaa	aga	gag	cgg	gtc	tat	acc	ctt	tac	ctt	gaa	aac	aaa	1445
Arg	Glu	Glu	Lys	Arg	Glu	Arg	Val	Tyr	Thr	Leu	Tyr	Leu	Glu	Asn	Lys	
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Lys	Lys	Glu	Leu	His	Glu	Leu	Ala	Glu	Arg	Gln	Lys	Phe	Val	Leu	Asp	
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Phe	His	Phe	Pro	Thr	Phe	Glu	Arg	Met	Lys	Tyr	Leu	Thr	Lys	Glu	Ile	
			335					340					345			
agc	gga	cga	att	tgg	gaa	aaa	tcg	att	gaa	agc	gcc	gat	ttt	ctg	caa	1589
Ser	Gly	Arg	Ile	Trp	Glu	Lys	Ser	Ile	Glu	Ser	Ala	Asp	Phe	Leu	Gln	
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Ile	Arg	Leu	Gly	Thr	Gly	Asn	Val	Ala	Ser	Ser	Tyr	Gln	Ile	Asn	Leu	
	365					370					375					
aac	ggc	gga	gat	ttg	gcc	aac	cg	gat	aca	gac	cat	ctc	ctt	gaa	caa	1685
Asn	Gly	Gly	Asp	Leu	Ala	Asn	Arg	Asp	Thr	Asp	His	Leu	Leu	Glu	Gln	
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acg	caa	aaa	atg	gaa	gag	gtc	tac	aga	gag	ctg	aaa	aat	gcg	ccg	atc	1733
Thr	Gln	Lys	Met	Glu	Glu	Val	Tyr	Arg	Glu	Leu	Lys	Asn	Ala	Pro	Ile	
				400					405					410		
act	gtg	aat	ctt	gcc	gaa	ggc	ccg	atg	ggc	gtc	gtc	gga	aaa	ttg	tcc	1781
Thr	Val	Asn	Leu	Ala	Glu	Gly	Pro	Met	Gly	Val	Val	Gly	Lys	Leu	Ser	
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His	Ser	Tyr	His	Asp	Leu	Arg	Phe	Val	Phe	Ile	Phe	Asp	Glu	Ala	Glu	
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Tyr	Gln	Glu	Trp	Glu	Trp	Met	Lys	Trp	Leu	Pro	His	Phe	Gln	Met	Pro	
460					465					470					475	
cat	att	tat	gcg	aaa	ggg	ttt	att	tac	aac	gaa	cag	acg	aga	gat	cag	1973
His	Ile	Tyr	Ala	Lys	Gly	Phe	Ile	Tyr	Asn	Glu	Gln	Thr	Arg	Asp	Gln	
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ctc	ctt	tca	agc	ata	tat	gag	att	ttg	aga	gaa	cgg	gat	tta	gat	gaa	2021
Leu	Leu	Ser	Ser	Ile	Tyr	Glu	Ile	Leu	Arg	Glu	Arg	Asp	Leu	Asp	Glu	
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Asn	Lys	Lys	Lys	Thr	Leu	Phe	Lys	Pro	His	Phe	Val	Phe	Ile	Ile	Thr	
		510					515					520				

10295.204.ST25.txt

aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly 525 530 535	2117
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys 540 545 550 555	2165
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu 560 565 570	2213
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro 575 580 585	2261
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc ccg Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg 590 595 600	2309
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro 605 610 615	2357
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp 620 625 630 635	2405
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu 640 645	2453
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn 655 660 665	2501
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr 670 675 680	2549
ggg tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597
gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys 700 705 710 715	2645
ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly 720 725 730	2693
acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu 735 740 745	2741
gcg tcc att aag agc gag ctg aag aaa agg cag cgg ctc ttt gat cag Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln 750 755 760	2789
tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys 765 770 775	2837
aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe 780 785 790 795	2885

10295.204.ST25.txt																
gcc	gag	ctg	aaa	agc	gaa	gaa	ccg	gaa	ttt	atc	cgc	gag	ctt	gtc	agt	2933
Ala	Glu	Leu	Lys	Ser	Glu	Glu	Pro	Glu	Phe	Ile	Arg	Glu	Leu	Val	Ser	
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gcg	gca	agg	atc	ggg	cga	agc	ctc	ggg	gtg	cac	tta	atc	ttg	gcg	acg	2981
Ala	Ala	Arg	Ile	Gly	Arg	Ser	Leu	Gly	Val	His	Leu	Ile	Leu	Ala	Thr	
			815					820					825			
caa	aaa	ccg	ggc	ggc	atc	atc	gat	gac	cag	att	tgg	agc	aac	tcc	aga	3029
Gln	Lys	Pro	Gly	Gly	Ile	Ile	Asp	Asp	Gln	Ile	Trp	Ser	Asn	Ser	Arg	
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ttc	aag	gtc	gcc	ttg	aag	gtg	cag	gat	gcg	aat	gac	agt	aaa	gag	atc	3077
Phe	Lys	Val	Ala	Leu	Lys	Val	Gln	Asp	Ala	Asn	Asp	Ser	Lys	Glu	Ile	
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ctc	aaa	aac	ggg	gat	gcg	gct	acc	atc	acg	gta	acg	ggc	cgc	ggc	tat	3125
Leu	Lys	Asn	Gly	Asp	Ala	Ala	Thr	Ile	Thr	Val	Thr	Gly	Arg	Gly	Tyr	
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ttg	caa	gtc	ggc	aac	aac	gag	gtg	tat	gaa	ctg	ttc	cag	tct	gca	tgg	3173
Leu	Gln	Val	Gly	Asn	Asn	Glu	Val	Tyr	Glu	Leu	Phe	Gln	Ser	Ala	Trp	
				880					885					890		
agc	gga	gcc	cct	tac	atg	gag	gac	ggc	tac	ggc	aca	gag	gat	gaa	gtg	3221
Ser	Gly	Ala	Pro	Tyr	Met	Glu	Asp	Gly	Tyr	Gly	Thr	Glu	Asp	Glu	Val	
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gcg	atc	gtc	aca	gat	acc	gga	tta	att	cct	tta	tca	gat	gtt	gat	gct	3269
Ala	Ile	Val	Thr	Asp	Thr	Gly	Leu	Ile	Pro	Leu	Ser	Asp	Val	Asp	Ala	
		910					915					920				
gat	cgc	gct	gcg	aaa	aaa	gag	gct	gtg	acg	gaa	att	tcg	gca	gtc	gtc	3317
Asp	Arg	Ala	Ala	Lys	Lys	Glu	Ala	Val	Thr	Glu	Ile	Ser	Ala	Val	Val	
	925					930					935					
gaa	caa	att	gaa	cgg	att	caa	gcg	gag	atg	gga	atc	gag	aag	ctc	ccg	3365
Glu	Gln	Ile	Glu	Arg	Ile	Gln	Ala	Glu	Met	Gly	Ile	Glu	Lys	Leu	Pro	
	940				945					950					955	
agc	cct	tgg	ctg	ccg	ccg	ctt	gaa	gaa	cgc	ata	ccg	aaa	acg	cgc	tat	3413
Ser	Pro	Trp	Leu	Pro	Pro	Leu	Glu	Glu	Arg	Ile	Pro	Lys	Thr	Arg	Tyr	
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ccg	tcg	gag	gaa	gcc	gat	gcc	ttt	aac	ttt	gcc	tat	atc	gat	gaa	cct	3461
Pro	Ser	Glu	Glu	Ala	Asp	Ala	Phe	Asn	Phe	Ala	Tyr	Ile	Asp	Glu	Pro	
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gaa	aag	caa	agc	cag	gag	ccg	atc	agc	tac	cgc	atg	atg	gaa	gac	ggc	3509
Glu	Lys	Gln	Ser	Gln	Glu	Pro	Ile	Ser	Tyr	Arg	Met	Met	Glu	Asp	Gly	
		990					995					1000				
aat	atc	ggc	atc	gtc	ggc	tcg	tca	ggc	tac	gga	aaa	tcc	ctg	aca		3554
Asn	Ile	Gly	Ile	Val	Gly	Ser	Ser	Gly	Tyr	Gly	Lys	Ser	Leu	Thr		
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gcc	acg	acg	ttc	atg	atg	agc	ttt	gcc	gaa	cag	tat	acg	ccg	gaa		3599
Ala	Thr	Thr	Phe	Met	Met	Ser	Phe	Ala	Glu	Gln	Tyr	Thr	Pro	Glu		
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gaa	ttg	cat	tac	tac	att	ttc	gac	ttt	ggc	aac	gga	acg	ctg	ctt		3644
Glu	Leu	His	Tyr	Tyr	Ile	Phe	Asp	Phe	Gly	Asn	Gly	Thr	Leu	Leu		
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ccg	ctt	gca	agg	ctt	ccg	cac	acc	gcg	gat	tat	ttc	ctg	atg	gac		3689
Pro	Leu	Ala	Arg	Leu	Pro	His	Thr	Ala	Asp	Tyr	Phe	Leu	Met	Asp		
	1050					1055					1060					

10295.204.ST25.txt

caa acg aga aaa atc gag aaa ttt atg gtc cgg atc aag gcg gaa Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu 1065 1070 1075	3734
atc gag cac agg aaa aat ctc ttc cgt gca aaa gaa atc agc cat Ile Glu His Arg Lys Asn Leu Phe Arg Ala Lys Glu Ile Ser His 1080 1085 1090	3779
atc aag atg tac aat gcg ctg aat gag gaa aag ctg ccg ttt att Ile Lys Met Tyr Asn Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile 1095 1100 1105	3824
ttc ata acg gtc gac aac ttt gac atc att aaa gac gaa atg cat Phe Ile Thr Val Asp Asn Phe Asp Ile Ile Lys Asp Glu Met His 1110 1115 1120	3869
gaa ctc gaa agc gaa ttt atc cag ttt tca cga gac ggc cag tcg Glu Leu Glu Ser Glu Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser 1125 1130 1135	3914
ctt gga att tat tta atc ctg acc gcg aca agg gtc aat gca atc Leu Gly Ile Tyr Leu Ile Leu Thr Ala Thr Arg Val Asn Ala Ile 1140 1145 1150	3959
aga cag tcg ctc ttg aac aac ctg aaa acg agg gtt gtc cac tat Arg Gln Ser Leu Leu Asn Asn Leu Lys Thr Arg Val Val His Tyr 1155 1160 1165	4004
ctg atg gat cag tct gaa gca tat tcg att atc gga agg ccg gaa Leu Met Asp Gln Ser Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu 1170 1175 1180	4049
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aac caa tac ttc gca caa atg ttt atg cct gtg gaa gcg gac aac Asn Gln Tyr Phe Ala Gln Met Phe Met Pro Val Glu Ala Asp Asn 1200 1205 1210	4139
gat atc gag ctg ttt gaa ggg atc aaa gcc gac att cag gcg atc Asp Ile Glu Leu Phe Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile 1215 1220 1225	4184
gca gaa cgc tcg gaa ggc atg aga aag ccg gcg cct gtg ccg atg Ala Glu Arg Ser Glu Gly Met Arg Lys Pro Ala Pro Val Pro Met 1230 1235 1240	4229
ctg ccg ctc gag ctt tcc gtc aca cag ttt gtg aga gat tat ccg Leu Pro Leu Glu Leu Ser Val Thr Gln Phe Val Arg Asp Tyr Pro 1245 1250 1255	4274
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act gtc gaa ccc gta tac ttt aat ctt gag aaa aat aag cac tgc Thr Val Glu Pro Val Tyr Phe Asn Leu Glu Lys Asn Lys His Cys 1275 1280 1285	4364
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atc atg ctc gag cac ctg ctt gac cat gac acg aaa aaa atc gcc Ile Met Leu Glu His Leu Leu Asp His Asp Thr Lys Lys Ile Ala 1305 1310 1315	4454

10295.204.ST25.txt

gtg ttt gat tcg ata gac aga ggg ctt tct caa tat gcg aca gag	4499
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gat caa atc agc tat cta gaa aca aaa gac gac att ctg ctc tgg	4544
Asp Gln Ile Ser Tyr Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp	
1335 1340 1345	
ctc gct gag acg gaa gaa att tgc cgg aca agg gaa gcg atg tat	4589
Leu Ala Glu Thr Glu Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr	
1350 1355 1360	
ttg gaa gcc gtt aaa caa gga gaa atc gcc aac ctt gat ttc tca	4634
Leu Glu Ala Val Lys Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser	
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Pro Met Val Phe Ile Val Asp Gly Ile Ser Arg Phe Gln Gln Thr	
1380 1385 1390	
atc gac gca tcg att cag gac aaa atg gcg atg ttc atg aaa tct	4724
Ile Asp Ala Ser Ile Gln Asp Lys Met Ala Met Phe Met Lys Ser	
1395 1400 1405	
tac gcc cat tta ggt ttc cac ttt ata cct gcc gga aat cac agc	4769
Tyr Ala His Leu Gly Phe His Phe Ile Pro Ala Gly Asn His Ser	
1410 1415 1420	
gag ttc aca aaa ggc tat gat tcg ctg aca agc gaa gtc aag cag	4814
Glu Phe Thr Lys Gly Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln	
1425 1430 1435	
gtc aga cac gcg atg cta ttg atg aaa aaa tcc gag cag aac ttg	4859
Val Arg His Ala Met Leu Leu Met Lys Lys Ser Glu Gln Asn Leu	
1440 1445 1450	
att cag ctc cca tat gaa cgc cag gag ccg gaa att ctg ccg ggc	4904
Ile Gln Leu Pro Tyr Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly	
1455 1460 1465	
ttt ggc tat atc gtt gaa aac ggc aaa gag agg aaa att caa att	4949
Phe Gly Tyr Ile Val Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile	
1470 1475 1480	
cct tta tgt gct gta gaa agg aag aaa gcg aaa tgacggaaca	4992
Pro Leu Cys Ala Val Glu Arg Lys Lys Ala Lys	
1485 1490	
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10295.204.ST25.txt

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<213> Bacillus licheniformis

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20 25 30His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
35 40 45Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
50 55 60Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
65 70 75 80Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
85 90 95Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
100 105 110Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
115 120 125Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
130 135 140Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
145 150 155 160Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
165 170 175Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
180 185 190Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
195 200 205Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
210 215 220Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
225 230 235 240Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
245 250 255

10295.204.ST25.txt

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
 260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
 275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
 290 295 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
 305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
 325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
 340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
 355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
 370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
 385 390 395 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
 405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
 420 425 430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
 435 440 445

Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
 450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
 465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
 485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
 500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
 515 520 525

10295.204.ST25.txt

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
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Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
 545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
 565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
 580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
 595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
 610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
 625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
 645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
 660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
 675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
 690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
 705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
 725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
 740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
 755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
 770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
 785 790 795 800

10295.204.ST25.txt

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 Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
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 Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
 835 840 845
 Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
 850 855 860
 Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
 865 870 875 880
 Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
 885 890 895
 Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
 900 905 910
 Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
 915 920 925
 Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
 930 935 940
 Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
 945 950 955 960
 Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
 965 970 975
 Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
 980 985 990
 Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
 995 1000 1005
 Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
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 Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
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 Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile
 1055 1060 1065

10295.204.ST25.txt

Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
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 Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
 1100 1105 1110
 Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
 1115 1120 1125
 Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
 1130 1135 1140
 Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
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 1160 1165 1170
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 Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
 1265 1270 1275
 Tyr Phe Asn Leu Glu Lys Asn Lys His Cys Leu Ile Met Gly Gln
 1280 1285 1290
 Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
 1295 1300 1305
 Leu Leu Asp His Asp Thr Lys Lys Ile Ala Val Phe Asp Ser Ile
 1310 1315 1320

Asp	Arg 1325	Gly	Leu	Ser	Gln	Tyr 1330	Ala	Thr	Glu	Asp	Gln 1335	Ile	Ser	Tyr
Leu	Glu 1340	Thr	Lys	Asp	Asp	Ile 1345	Leu	Leu	Trp	Leu	Ala 1350	Glu	Thr	Glu
Glu	Ile 1355	Cys	Arg	Thr	Arg	Glu 1360	Ala	Met	Tyr	Leu	Glu 1365	Ala	Val	Lys
Gln	Gly 1370	Glu	Ile	Ala	Asn	Leu 1375	Asp	Phe	Ser	Pro	Met 1380	Val	Phe	Ile
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Gln	Asp 1400	Lys	Met	Ala	Met	Phe 1405	Met	Lys	Ser	Tyr	Ala 1410	His	Leu	Gly
Phe	His 1415	Phe	Ile	Pro	Ala	Gly 1420	Asn	His	Ser	Glu	Phe 1425	Thr	Lys	Gly
Tyr	Asp 1430	Ser	Leu	Thr	Ser	Glu 1435	Val	Lys	Gln	Val	Arg 1440	His	Ala	Met
Leu	Leu 1445	Met	Lys	Lys	Ser	Glu 1450	Gln	Asn	Leu	Ile	Gln 1455	Leu	Pro	Tyr
Glu	Arg 1460	Gln	Glu	Pro	Glu	Ile 1465	Leu	Pro	Gly	Phe	Gly 1470	Tyr	Ile	Val
Glu	Asn 1475	Gly	Lys	Glu	Arg	Lys 1480	Ile	Gln	Ile	Pro	Leu 1485	Cys	Ala	Val
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10295.204.ST25.txt

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(71) Applicant (for all designated States except US):
NOVOZYMES A/S [DK/DK]; Krogshøjvej 36, DK-2880
Bagsværd (DK).

(72) Inventors; and

(75) Inventors/Applicants (for US only): ANDERSEN,
Jens, Tønne [DK/DK]; Alfred Christensens Vej 35,
DK-2850 Nærum (DK). JØRGENSEN, Steen, Troels
[DK/DK]; Prunusvej 5, DK-3450 Allerød (DK). RAS-
MUSSEN, Michael, Dolbjerg [DK/DK]; Syvbjergvej
151, DK-2625 Vallensbæk (DK). OLSEN, Peter, Bjarke
[DK/DK]; Svendborggade 8, 4 tv, DK-2100 Copenhagen
Ø (DK). CLAUSEN, Ib, Groth [DK/DK]; Fyrrestien 6,
DK-3400 Hillerød (DK).

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CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE,
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(84) Designated States (regional): ARIPO patent (GH, GM,
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European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,
SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,
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Published:

— with international search report

(88) Date of publication of the international search report:
18 March 2004

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: BACILLUS LICHENIFORMIS MUTANT HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell comprising a mutation (deletion) in one or more genes encoding polypep-
tides involved in sporulation wherein the mutant host cell expresses at least 5% less of the one or more polypeptides involved in
sporulation than the parent host cell, when cultivated under comparable conditions. The mutant host cell is used for producing het-
erologous polypeptides.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/DK 03/00200

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/75 C12N1/21 C07K14/32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 03185 A (NOVONORDISK AS ;PRIEST FERGUS G (GB); FLEMING ALASTAIR B (GB); TAN) 30 January 1997 (1997-01-30) the whole document	1-21
X	--- FLEMING A B ET AL: "Extracellular enzyme synthesis in a sporulation-deficient strain of Bacillus licheniformis." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 61, no. 11, November 1995 (1995-11), pages 3775-3780, XP002902964 ISSN: 0099-2240 abstract	1-21
X	--- WO 98 22598 A (NOVO NORDISK BIOTECH INC) 28 May 1998 (1998-05-28) page 6, line 8 - line 11; claims 1,2,17 --- -/--	1-21

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

15 July 2003

Date of mailing of the international search report

28. 10. 2003

Name and mailing address of the ISA
European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Ida Christensen

INTERNATIONAL SEARCH REPORT

International Application No
PCT/DK 03/00200

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO 02 00907 A (JOERGENSEN STEEN TROELS ;OLSEN CARSTEN (DK); NOVOZYMES AS (DK); AN) 3 January 2002 (2002-01-03) claims -----</p>	6,7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 03/00200

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-21 (partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 2.

Invention 2 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 4.

Invention 3: claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 6

Invention 4 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No:

etc....

etc....

etc....

Invention 96 :claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 191.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/DK 03/00200

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9703185	A	30-01-1997	AU 6353896 A	10-02-1997
			CN 1190434 A	12-08-1998
			WO 9703185 A1	30-01-1997
			EP 0837925 A1	29-04-1998
			JP 11509096 T	17-08-1999

WO 9822598	A	28-05-1998	AT 246251 T	15-08-2003
			AU 5445098 A	10-06-1998
			DE 69723855 D1	04-09-2003
			EP 0941349 A1	15-09-1999
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